

OM protein - protein search, using sw model  
Run on: May 12, 2006, 20:33:31 ; Search time 187 Seconds  
(without alignments)  
549,811 Million cell updates/sec

Title: US-10-063-518-14  
Perfect score: 1195  
Sequence: 1 MNHLPDMEALTGSSQSHR.....EAGSEAEKQDSEKPLEL 234  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
2443163 seqs, 439378781 residues  
Total number of hits satisfying chosen parameters: 2443163  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : A\_Geneseq\_21:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAU29056	standard;	protein;	234	AA.	
DE	Human PRO	polypeptide	sequence	#33.		
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 1195;	DB 4;	Length 234;	
Best Local Similarity		100.0%;	Pred. No. 1.5e-131;			
RESULT 2						
ID	AAU39929	standard;	protein;	234	AA.	
DE	Human polypeptide	SEQ ID NO 3074.				
PN	WO200153312-A1.					
PD	26-JUL-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match		100.0%;	Score 1195;	DB 4;	Length 234;	
Best Local Similarity		100.0%;	Pred. No. 1.5e-131;			
RESULT 3						
ID	AAU87532	standard;	protein;	234	AA.	
DE	Human PRO1864.					
PN	WO20016318-A2.					
PD	08-MAR-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 1195;	DB 4;	Length 234;	
Best Local Similarity		100.0%;	Pred. No. 1.5e-131;			
RESULT 4						
ID	ABG95857	standard;	protein;	234	AA.	
DE	Human secreted/transmembrane	protein PRO1864.				
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 1195;	DB 5;	Length 234;	
Best Local Similarity		100.0%;	Pred. No. 1.5e-131;			
RESULT 5						
ID	ABU84847	standard;	protein;	234	AA.	
DE	Human PRO1864	protein sequence	SEQ ID NO:62.			
PN	WO2002006890-A2.					
PD	03-JAN-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 1195;	DB 5;	Length 234;	
Best Local Similarity		100.0%;	Pred. No. 1.5e-131;			
RESULT 6						
ID	ABU95453	standard;	protein;	234	AA.	
DE	Human angiogenesis	related protein PRO1864	SEQ ID NO: 62.			

PN WO200208284-A2.

PD 31-JAN-2002.

PA (GETH ) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

Query Match

Best Local Similarity 100.0%;

Score 1195;

DB 5;

Length 234;

Pred. No. 1.5e-131;

RESULT 7

ID ABU58432

standard;

protein;

234

AA.

DE Human PRO

polypeptide

#33.

PN US2003021272-A1.

PD 06-FEB-2003.

Query Match

Best Local Similarity 100.0%;

Score 1195;

DB 6;

Length 234;

Pred. No. 1.5e-131;

RESULT 8

ID ABU87980

standard;

protein;

234

AA.

DE Novel human

secreted and transmembrane

protein PRO1864.

PN US2003032127-A1.

PD 13-FEB-2003.

Query Match

Best Local Similarity 100.0%;

Score 1195;

DB 6;

Length 234;

Pred. No. 1.5e-131;

RESULT 9

ID ABU84295

standard;

protein;

234

AA.

DE Human secreted/transmembrane

protein (PRO) #33.

PN US2003032112-A1.

PD 13-FEB-2003.

Query Match

Best Local Similarity 100.0%;

Score 1195;

DB 6;

Length 234;

Pred. No. 1.5e-131;

RESULT 10

ID ABR66169

standard;

protein;

234

AA.

DE Human secreted polypeptide

PRO1864, SEQ ID NO:66.

PN US2003027278-A1.

PD 06-FEB-2003.

Query Match

Best Local Similarity 100.0%;

Score 1195;

DB 6;

Length 234;

Pred. No. 1.5e-131;

RESULT 11

ID ABR65559

standard;

protein;

234

AA.

DE Human secreted polypeptide

PRO1864, SEQ ID NO:66.

PN US2003036159-A1.

PD 20-FEB-2003.

Query Match

Best Local Similarity 100.0%;

Score 1195;

DB 6;

Length 234;

Pred. No. 1.5e-131;

RESULT 12

ID ABU99499

standard;

protein;

234

AA.

DE Human secreted/transmembrane

protein (PRO) #33.

PN US2003040070-A1.

PD 27-FEB-2003.

Query Match

Best Local Similarity 100.0%;

Score 1195;

DB 6;

Length 234;

Pred. No. 1.5e-131;

RESULT 13

ID ABU82738

standard;

protein;

234

AA.

DE Human PRO

polypeptide

#33.

PN US2003032113-A1.

PD 13-FEB-2003.

Query Match

Best Local Similarity 100.0%;

Score 1195;

DB 6;

Length 234;

Pred. No. 1.5e-131;

RESULT 14

ID ABU89859

standard;

protein;

234

AA.

DE Novel human

secreted and transmembrane

protein PRO1864.

PN US2003036147-A1.

PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 15  
ID ABR68108 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 16  
ID ABU96161 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 17  
ID ABU92592 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 18  
ID ABO08669 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 19  
ID ABO02721 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 20  
ID ABR74875 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 21  
ID ABR94637 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 22  
ID ABU85610 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 23  
ID ABU98770 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003033153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 24  
ID ABU97985 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 25  
ID ABU91691 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 26  
ID ABU9384 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 27  
ID ABU86225 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 28  
ID ABU67438 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 29  
ID ABU80466 standard; protein; 234 AA.  
DE Human PRO protein #33.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 30  
ID ABU90882 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 31  
ID ABO33941 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein PRO1864.  
PN US2003009013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 32  
ID ABR99384 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 33  
ID ABR98774 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 34  
ID ABO16297 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003027267-A1.

PD 06-FEB-2003. 100.0%; Score 1195; DB 6; Length 234;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 35  
ID ABR92197 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 36  
ID ABO1863 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 37  
ID ABR78259 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 38  
ID ABR3937 standard; protein; 234 AA.  
DE Human prostate selective polypeptide PR340.  
PN WO2003014298-A2.  
PD 20-FEB-2003.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 39  
ID ABR71958 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 40  
ID ABR8495 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 41  
ID ABO00134 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 42  
ID ABO11466 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 43  
ID ABO02111 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 44  
ID ABR8865 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036133-A1.

PD 20-FEB-2003. 100.0%; Score 1195; DB 6; Length 234;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 45  
ID ABR83380 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 46  
ID ABO06181 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 47  
ID ABR59217 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 48  
ID ABO09279 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 49  
ID ABO19143 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 50  
ID ABO11161 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 51  
ID ABR6779 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 52  
ID ABO15992 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 53  
ID ABO13698 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 54  
ID ABR71512 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 55  
ID ABU65601 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein, SEQ ID 66.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 56  
ID ABO07449 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 57  
ID ABO03636 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 58  
ID ABR67084 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 59  
ID ABO15687 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 60  
ID ABUS5968 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein, PRO1864.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 61  
ID ABU72293 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 62  
ID ABU65296 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 63  
ID ABU95241 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 64  
ID ABU71144 standard; protein; 234 AA.  
DE Human PRO1864 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 65  
ID ABO07754 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 66  
ID ABR69995 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 67  
ID ABR69328 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 68  
ID ABO01469 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 69  
ID ABU81271 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 70  
ID ABR60068 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 71  
ID ABR58287 standard; protein; 234 AA.  
DE BCU0092 protein #SEQ ID 20.  
PN WO2003029421-A2.  
PD 10-APR-2003.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 72  
ID ABU90966 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 73  
ID ABR67803 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 74  
ID ABR65191 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027268-A1.  
PD 06-FEB-2003.



Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 75  
ID ABR68413 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 76  
ID ABR71825 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US200302135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 77  
ID ABR85305 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 78  
ID ABR8995 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 79  
ID ABR83075 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 80  
ID ABR94931 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US200303123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 81  
ID ABR90479 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 82  
ID ABR83990 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 83  
ID ABR93641 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 84  
ID ABR64886 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 85  
ID ABO27287 standard; protein; 234 AA.  
DE Human secreted/transmembrane polypeptide PRO1864.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 86  
ID ABR68718 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 87  
ID ABO6534 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 88  
ID ABR99079 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 89  
ID ABR56963 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 90  
ID ABR8915 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 91  
ID ABR82202 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 92  
ID ABR87213 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 93  
ID ABR83685 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 94  
ID ABO08059 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 95

ID ABU92482 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein PRO1864.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 96  
ID ABU81770 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 97  
ID ABU65934 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 98  
ID ABU81152 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 99  
ID ABR59763 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 100  
ID ABU93951 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 101  
ID ABU99804 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 102  
ID ABR66474 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 103  
ID ABR90892 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 104  
ID ABO53267 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 105  
ID ABU94319 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 106  
ID ABU79201 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 107  
ID ABU86530 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 108  
ID ABU86835 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 109  
ID ABU94624 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 110  
ID ABO04551 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 111  
ID ABR70300 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 112  
ID ABU98465 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 113  
ID ABR65864 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 114  
ID ABR64581 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 115  
ID ABU79506 standard; protein; 234 AA.

DE Human PRO polypeptide #33.  
PN US200303210-A1.  
13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 116  
ID ABU92897 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036142-A1.  
20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 117  
ID ABU95856 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003036145-A1.  
20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 118  
ID ABU91076 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036154-A1.  
20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 119  
ID ABU90169 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036153-A1.  
20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 120  
ID AB00984 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044931-A1.  
06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 121  
ID AB010856 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036150-A1.  
20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 122  
ID ABR70910 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040069-A1.  
27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 123  
ID AB098269 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2002183493-A1.  
05-DEC-2002.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
PA (GENENTECH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 124  
ID ABU87518 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003022293-A1.  
30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 125  
ID ABU91386 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032128-A1.

PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 126  
ID ABU9274 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003036634-A1.  
20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
PA (GENENTECH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 127  
ID ABU84600 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032116-A1.  
13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 128  
ID ABR69690 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003032122-A1.  
13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 129  
ID ABU8067 standard; protein; 234 AA.  
DE Human PRO protein #33.  
PN US2003036139-A1.  
20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 130  
ID ABU82481 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2002183494-A1.  
05-DEC-2002.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
PA (GENENTECH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 131  
ID ABU93336 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003017541-A1.  
23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 132  
ID AB009889 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003017543-A1.  
20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 133  
ID AB008974 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036152-A1.  
20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 134  
ID ABU96445 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003027993-A1.  
06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
PA (GENENTECH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
Pred. No. 1.5e-131;  
RESULT 135  
ID ABU10542 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein #33.  
PN US2002127584-A1.

PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;  
RESULT 136  
ID ABU72115 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 137  
ID ABU95551 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 138  
ID ABU96760 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 139  
ID ABR70605 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 140  
ID ABO04956 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 141  
ID ABO08364 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 142  
ID ABO05571 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 143  
ID ABR73960 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 144  
ID ABR95552 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 145  
ID ABR80849 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 146  
ID ABR81154 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 147  
ID ABM00850 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 148  
ID ABR8452 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 149  
ID ABM77273 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 150  
ID ABO28757 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 151  
ID ABO31502 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 152  
ID ABM07919 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 153  
ID ABO40399 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 154  
ID ABO35824 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.

PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 155  
ID ABO43963 standard; protein: 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 156  
ID ADA77818 standard; protein: 234 AA.  
DE Human secreted/cranmembrane protein (PRO) #33.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 157  
ID ABM24758 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 158  
ID ABO03026 standard; protein: 234 AA.  
DE Human secreted/cranmembrane protein (PRO) #33.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 159  
ID ABR90282 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 160  
ID ABM17196 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 161  
ID ABR94942 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 162  
ID ABR95247 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 163  
ID ADB17071 standard; protein: 234 AA.  
DE Human transmembrane PRO polypeptide (SeqID 14).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 164  
ID ABO21485 standard; protein: 234 AA.  
DE Human secreted/cranmembrane protein (PRO) #33.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 165  
ID ABR97749 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 166  
ID ABR87537 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 167  
ID ABR77578 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 168  
ID ABM27808 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 169  
ID ABO06089 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 170  
ID ABO03595 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 171  
ID ABM35046 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 172  
ID ABR26283 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 173  
ID ABO48065 standard; protein: 234 AA.

DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 174  
ID ABR92807 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 175  
ID ABO24568 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 176  
ID ABO11579 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 177  
ID ABO2680 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 178  
ID ABO15976 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 179  
ID ABO27537 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 180  
ID ABO23028 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 181  
ID ABO07004 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 182  
ID ABO21098 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 183  
ID ABO09444 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 184  
ID ABO41314 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 185  
ID ABO36129 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 186  
ID ABO43658 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 187  
ID ABO76358 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 188  
ID ABO76054 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104546-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 189  
ID ABO25673 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 190  
ID ABO25978 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 191  
ID ABO03331 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 192  
ID ABO02416 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 193  
ID ABO44245 standard; protein; 234 AA.  
DE Human secreted/transmembrane polypeptide PRO 1864.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 194  
ID ABR90587 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 195  
ID ABR73655 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 196  
ID ABO16907 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 197  
ID ABR94332 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 198  
ID ABR75839 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 199  
ID ABR71215 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 200  
ID ABR93112 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 201  
ID ABR93417 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 202  
ID ABR87842 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 203  
ID ABO27842 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 204  
ID ABO29977 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 205  
ID ABO33186 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 206  
ID ABO04874 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 207  
ID ABO08834 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 208  
ID ABO36434 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 209  
ID ABO35519 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 210  
ID ABO39484 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 211  
ID ABM10359 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 212  
ID ABM11884 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 213  
ID ABO52030 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 214  
ID ABO52335 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 215  
ID ADA19876 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 216  
ID ABO23653 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 217  
ID ADB17259 standard; protein; 234 AA.  
DE Human transmembrane PRO polypeptide (SeqID 14).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 218  
ID ABR97139 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 219  
ID ABR86927 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 220  
ID ABM10969 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 221  
ID ABM28113 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 222  
ID ABO32112 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068733-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 223  
ID ABM15239 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068692-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 224  
ID ABM06394 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068709-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 225  
ID ABM04205 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068716-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 226  
ID ABM22318 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068740-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 227  
ID ABM07614 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068751-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 228  
ID ABO40704 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068684-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 229



ID ABM35351 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073179-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 230  
ID ABM33114 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 231  
ID ABO52640 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 232  
ID ABO50200 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 233  
ID ABG9194 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040055-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 234  
ID ABO04246 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 235  
ID ABO05876 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 236  
ID ABM18416 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 237  
ID ABR97444 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 238  
ID ABR0544 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 239  
ID ABM01155 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 240  
ID ABR88757 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 241  
ID ABM13409 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 242  
ID ABM20793 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 243  
ID ABO41924 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 244  
ID ABO42534 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 245  
ID ABM10054 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 246  
ID ABO38569 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 247  
ID ABM32809 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

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RESULT 248
ID  ABM22623 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003087373-A1.
PD  08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM74834 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003096353-A1.
PD  22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ADA79610 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003073173-A1.
PD  17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABR96224 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003054458-A1.
PD  20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM02375 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003059886-A1.
PD  27-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABR86317 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003049758-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABR86622 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003049772-A1.
PD  13-MAR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM16586 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003064448-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM23638 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003064456-A1.
PD  03-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABO23062 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003068693-A1.
PD  10-APR-2003.

PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM23843 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003068735-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM23233 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003068753-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM22013 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003068742-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABO37654 standard; protein; 234 AA.
DE  Human secreted/transmembrane protein (PRO) #33.
PN  US2003068756-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM28418 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003082715-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM28723 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003082716-A1.
PD  01-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM66367 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003068737-A1.
PD  10-APR-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM75749 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003104547-A1.
PD  05-JUN-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
ID  ABM34029 standard; protein; 234 AA.
DE  Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN  US2003096359-A1.
PD  22-MAY-2003.
PA  (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD  10-APR-2003.
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RESULT 267
ID ABM34334 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US200310061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 268
ID ABO20265 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 269
ID ABO21180 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 270
ID ABO22095 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 271
ID ADA20048 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 272
ID ABO34173 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 273
ID ABR96529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 274
ID ABR85707 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 275
ID ABR9689 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 276
ID ABM00545 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 277
ID ABM00240 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 278
ID ABO29672 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 279
ID ABM23538 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 280
ID ABM29333 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 281
ID ABO38264 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 282
ID ABO45564 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 283
ID ABM2048 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 284
ID ADA81337 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 285
ID ABO16602 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
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Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 286  
ID ABO18228 standard; protein; 234 AA.  
DE Human secreted/cytoplasmic protein (PRO) #33.  
PN US200304920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 287  
ID ABO22655 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 288  
ID ABO22960 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003054461-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 289  
ID ABR92502 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 290  
ID ABR81459 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 291  
ID ABM77893 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 292  
ID ABR89672 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 293  
ID ABM26588 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 294  
ID ABM13714 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 295  
ID ABO28452 standard; protein; 234 AA.  
DE Human secreted/cytoplasmic protein (PRO) #33.  
PN US2003064460-A1.

PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 296  
ID ABO30282 standard; protein; 234 AA.  
DE Human secreted/cytoplasmic protein (PRO) #33.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 297  
ID ABM07309 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 298  
ID ABM03900 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 299  
ID ABO37044 standard; protein; 234 AA.  
DE Human secreted/cytoplasmic protein (PRO) #33.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 300  
ID ABO41619 standard; protein; 234 AA.  
DE Human secreted/cytoplasmic protein (PRO) #33.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 301  
ID ABO35214 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 302  
ID ABM25063 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 303  
ID ABO47455 standard; protein; 234 AA.  
DE Human secreted/cytoplasmic protein (PRO) #33.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 304  
ID ABO47760 standard; protein; 234 AA.  
DE Human secreted/cytoplasmic protein (PRO) #33.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 305  
ID ABO48370 standard; protein; 234 AA.  
DE Human secreted/cranmembrane protein (PRO) #33.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 306  
ID ABO51420 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 307  
ID ABO51725 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 308  
ID ABO50505 standard; protein; 234 AA.  
DE Human secreted/cranmembrane protein (PRO) #33.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 309  
ID ABR79629 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 310  
ID ABM16891 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 311  
ID ABO17923 standard; protein; 234 AA.  
DE Human secreted/cranmembrane protein (PRO) #33.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 312  
ID ABO20875 standard; protein; 234 AA.  
DE Human secreted/cranmembrane protein (PRO) #33.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 313  
ID ABR96834 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 314  
ID ABM12189 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 315  
ID ABM16281 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 316  
ID ABM24148 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 317  
ID ABM14629 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 318  
ID ABM04510 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 319  
ID ABM06699 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 320  
ID ABM09139 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 321  
ID ABO39179 standard; protein; 234 AA.  
DE Human secreted/cranmembrane protein (PRO) #33.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 322  
ID ABM75444 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 323  
ID ABM25368 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104541-A1.  
PD 05-JUN-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 324  
ID ABL19878 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 325  
ID ABO46784 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 326  
ID ABO47089 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 327  
ID ADA83135 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 328  
ID ABR71520 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 329  
ID ABR72130 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 330  
ID ABR98469 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 331  
ID ABO06639 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 332  
ID ABR84792 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 333  
ID ABR73350 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054467-A1.

PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 334  
ID ABR76444 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 335  
ID ABR73045 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 336  
ID ABL18111 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 337  
ID ABO20570 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 338  
ID ABO25313 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 339  
ID ABO25618 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 340  
ID ABR94027 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003058879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 341  
ID ABR79934 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 342  
ID ABL11274 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 343

ID ABO32881 standard; protein: 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 344  
ID ABO30587 standard; protein: 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 345  
ID ABO30892 standard; protein: 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 346  
ID ABO27198 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 347  
ID ABO29943 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 348  
ID ABO05479 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 349  
ID ABO15544 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 350  
ID ABO08529 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 351  
ID ABO42229 standard; protein: 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 352  
ID ABO37959 standard; protein: 234 AA.

DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 353  
ID ABO45869 standard; protein: 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 354  
ID ABO66672 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 355  
ID ABO20178 standard; protein: 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 356  
ID ABO19573 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 357  
ID ABO49285 standard; protein: 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 358  
ID ABO49590 standard; protein: 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 359  
ID ABO478430 standard; protein: 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 360  
ID ABO88147 standard; protein: 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 361  
ID ABO00345 standard; protein: 234 AA.  
DE Human secreted/transmembrane polypeptide PRO 1864.  
PN US2003027992-A1.

PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 362  
ID ABM26893 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 363  
ID ABM03290 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 6; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 364  
ID ABO39789 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 365  
ID ABO49895 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 366  
ID ABO50810 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 367  
ID ABO5266 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 368  
ID ABR74570 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 369  
ID ABR77049 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 370  
ID AMM17806 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 371

ID ABR95857 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 372  
ID ABO21790 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 373  
ID ABO19960 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 374  
ID ABO24263 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 375  
ID ABR86012 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 376  
ID ABM10664 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 377  
ID ABM76663 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 378  
ID ABR89367 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 379  
ID ABM12494 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 380  
ID ABM05784 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068717-A1.  
PD 10-APR-2003.



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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 381
ID ABO34909 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 382
ID ABM02985 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 383
ID ABM18963 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 384
ID ABM19268 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 385
ID ABO46479 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 386
ID ABO48980 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 387
ID ABRE9023 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 388
ID ABRE9062 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 389
ID ABR72435 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 390
ID ABR74265 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 391
ID ABO18533 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 392
ID ABR80239 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 393
ID ABM01460 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 394
ID ABM02070 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 395
ID ABR87232 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 396
ID ABM12799 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 397
ID ABM30553 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 398
ID ABM24453 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 399
ID ABO29367 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
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PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 400  
ID ABO31197 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068710-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 401  
ID ABM14324 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 402  
ID ABM09749 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 403  
ID ABO38874 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 404  
ID ABM34639 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 405  
ID ABO03941 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 406  
ID ABO03941 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 407  
ID ABO10411 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 408  
ID ABR77654 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 409  
ID ABR78864 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 410  
ID ABO23958 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 411  
ID ABR93722 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 412  
ID ABM01765 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 413  
ID ABM78188 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003048764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 414  
ID ABR89977 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 415  
ID ABM27503 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 416  
ID ABM13104 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 417  
ID ABO31807 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 418  
ID ABM14019 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068683-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 419  
ID ABM08224 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 420  
ID ABO40094 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068681-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 421  
ID ABM74529 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 422  
ID ABM33724 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 423  
ID ABM20183 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 424  
ID ABO48675 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 425  
ID ABR72740 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 426  
ID ABO15382 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 427  
ID ABR65097 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 428  
ID ABO15077 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 429  
ID ABO17212 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 430  
ID ABM17501 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 431  
ID ABR85402 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 432  
ID ABM76968 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 433  
ID ABO28147 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 434  
ID ABM22928 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 435  
ID ABM30248 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 436  
ID ABM21708 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 437  
ID ABM21403 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 438  
ID ABM14934 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 439  
ID ABO41009 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 440  
ID ABO36739 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 441  
ID ABO37349 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 442  
ID ABM75139 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 443  
ID ABM33419 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003096357-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 444  
ID ABO46174 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 445  
ID ADA82501 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003048755-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 446  
ID ADB8587 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003049735-A1.

PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 447  
ID ABM31773 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 448  
ID ABM31163 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 449  
ID ADB85809 standard; protein; 234 AA.  
DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 450  
ID ABM32078 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 451  
ID ABM32383 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 452  
ID ADB68266 standard; protein; 234 AA.  
DE Human PRO1864 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 453  
ID ADB68073 standard; protein; 234 AA.  
DE Human PRO1864 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 454  
ID ABM31468 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 455  
ID ABM30858 standard; protein; 234 AA.  
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 456				
ID	ADBG0690 standard; protein; 234 AA.			
DE	Novel human secreted and transmembrane protein PRO1864.			
PN	US2003083473-A1.			
PD	01-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 457				
ID	ADC06970 standard; protein; 234 AA.			
DE	Human PRO1864 protein.			
PN	US2003060602-A1.			
PD	27-MAR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 458				
ID	ADC17149 standard; protein; 234 AA.			
DE	Mammalian PRO polypeptide (segid 14).			
PN	US2003065143-A1.			
PD	03-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 459				
ID	ADC14847 standard; protein; 234 AA.			
DE	Novel human secreted and transmembrane protein PRO1864.			
PN	US2003073208-A1.			
PD	17-APR-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 460				
ID	ADC23242 standard; protein; 234 AA.			
DE	Novel human secreted and transmembrane protein PRO1864.			
PN	US2003138882-A1.			
PD	24-JUL-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 461				
ID	ADD05539 standard; protein; 234 AA.			
DE	Human secreted/transmembrane protein (PRO) #33.			
PN	US2003087376-A1.			
PD	08-MAY-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 462				
ID	ADD10351 standard; protein; 234 AA.			
DE	Human secreted/transmembrane PRO polypeptide #31.			
PN	US2003105011-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 463				
ID	ADD11311 standard; protein; 234 AA.			
DE	Human secreted/transmembrane PRO polypeptide #31.			
PN	US2003105013-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 464				
ID	ADD37104 standard; protein; 234 AA.			
DE	Human secreted/transmembrane PRO polypeptide #31.			
PN	US2003105012-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 465				
ID	ADD37104 standard; protein; 234 AA.			
DE	Human secreted/transmembrane PRO polypeptide #31.			
PN	US2003105012-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 466				
ID	ADD37104 standard; protein; 234 AA.			
DE	Human secreted/transmembrane PRO polypeptide #31.			
PN	US2003105012-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 467				
ID	ADD37104 standard; protein; 234 AA.			
DE	Human secreted/transmembrane PRO polypeptide #31.			
PN	US2003105012-A1.			
PD	05-JUN-2003.			
PA	(GETH) GENENTECH INC.			
Query Match	100.0%;	Score 1195;	DB 7;	Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.5e-131;		
RESULT 468				
ID	ADD37104 standard; protein; 234 AA.			
DE	Human secreted/transmembrane PRO polypeptide #31.			
PN	US200310			

Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 465		
ID	ADG06018 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003105298-A1.	
PD	05-JUN-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 466		
ID	ADG01019 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003078387-A1.	
PD	24-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 467		
ID	ADG08572 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180793-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 468		
ID	ADG02534 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003207397-A1.	
PD	06-NOV-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 469		
ID	ADG01241 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003207399-A1.	
PD	06-NOV-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 470		
ID	ADP95416 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003207398-A1.	
PD	06-NOV-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 471		
ID	ADP95193 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180795-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 472		
ID	ADG12231 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003207392-A1.	
PD	06-NOV-2003.	
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 473		
ID	ADH24046 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180918-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 474		
ID	ADH24046 standard; protein; 234 AA.	
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180918-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%;	Score 1195; DB 7; Length 234;
Best Local Similarity	100.0%;	Pred. No.1.5e-131;
RESULT 474		

ID ADH34072 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 475  
ID ADH29905 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 476  
ID ADH2876 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 477  
ID ADH08891 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 478  
ID ADG85280 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 479  
ID ADH24556 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 480  
ID ADH37412 standard; protein; 234 AA.  
DE Human secreted and transmembrane protein PRO1864.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 481  
ID ADH02001 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 482  
ID ADH37582 standard; protein; 234 AA.  
DE Human secreted and transmembrane protein PRO1864.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 483  
ID ADG85620 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 484  
ID ADH24216 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 485  
ID ADH38510 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 486  
ID ADG83631 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 487  
ID ADH29439 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 488  
ID ADH27555 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 489  
ID ADH37752 standard; protein; 234 AA.  
DE Human secreted and transmembrane protein PRO1864.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 490  
ID ADH37929 standard; protein; 234 AA.  
DE Human secreted and transmembrane protein PRO1864.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 491  
ID ADH57349 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 492  
ID ADH53491 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.

PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 493  
ID ADH985361 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 494  
ID ADH51997 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 495  
ID ADH49852 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 496  
ID AD125362 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 497  
ID ADH90155 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 498  
ID AD125532 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 499  
ID ADH97706 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 500  
ID AD103554 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 501  
ID AD11911 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 502  
ID ADH98985 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 503  
ID ADH98386 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 504  
ID AD11061 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 505  
ID AD11571 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 506  
ID ADH98216 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 507  
ID ADH98556 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 508  
ID ADH98046 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 509  
ID AD105034 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 7; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 510  
ID AD10384 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181654-A1.  
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 511
ID AD104779 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 512
ID ADH78233 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 513
ID AD119577 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 514
ID ADH90325 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 515
ID AD103044 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 516
ID ADH77893 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 517
ID ADH97876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 518
ID AD101261 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 519
ID AD101956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 520
ID AD103214 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 521
ID AD111401 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 522
ID AD102303 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 523
ID AD111741 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 524
ID AD105378 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 525
ID ADH79450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 526
ID AD119407 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 527
ID AD105208 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 528
ID ADH79620 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 529
ID AD101956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
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Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 529
ID ADI01446 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 530
ID ADI01616 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 531
ID ADI01786 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 532
ID ADH79790 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 533
ID ADI04608 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 534
ID ADI02744 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 535
ID ADH78063 standard; protein; 234 AA.
DE Human PRO polypeptide #.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 536
ID ADI25702 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 537
ID ADI25872 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 538
ID ADK65384 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 539
ID ADH98726 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 540
ID ADH79967 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 541
ID ADI32672 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 542
ID ADM30206 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 543
ID ADP3698 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 544
ID ADC52152 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 545
ID ADA41312 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 546
ID ADE74203 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.5e-131;
RESULT 547
ID ADE74815 standard; protein; 234 AA.
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DE Human secreted/transmembrane protein (PRO) #33.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 548  
ID ADF96028 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 549  
ID ADG04299 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 550  
ID ADG00459 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 551  
ID ADH06584 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 552  
ID ADH06414 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 553  
ID ADG68935 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 554  
ID ADH27725 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 555  
ID ADH25066 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 556  
ID ADH33698 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 557  
ID ADG82715 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 558  
ID ADH02341 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 559  
ID ADH07948 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 560  
ID ADG69345 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 561  
ID ADH39166 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 562  
ID ADH25996 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 563  
ID ADG83906 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 564  
ID ADG85450 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 565  
ID ADH06244 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 566  
ID ADH30074 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 567  
ID ADH2486 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 568  
ID ADH32965 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 569  
ID ADG69515 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 570  
ID ADH07778 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 571  
ID ADG85790 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 572  
ID ADH39336 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 573  
ID ADH33528 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 574  
ID ADH33868 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 575  
ID ADH01078 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 576  
ID ADG69685 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 577  
ID ADH02171 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 578  
ID ADG69175 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 579  
ID ADG85960 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 580  
ID ADH2486 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 581  
ID ADH39513 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 582  
ID ADH02511 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 583  
ID ADG69005 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;

RESULT 584  
ID ADH07608 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 585  
ID ADH66130 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 586  
ID ADH24726 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 587  
ID ADH25774 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 588  
ID ADH38340 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 589  
ID ADH57179 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 590  
ID ADH43495 standard; protein; 234 AA.  
DE Human PRO polypeptide #31.  
PN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 591  
ID ADH52167 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 592  
ID ADH45533 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 593  
ID ADH99103 standard; protein; 234 AA.

ID ADH90495 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 594  
ID ADI11231 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 595  
ID ADH98896 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 596  
ID ADI02126 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003190699-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 597  
ID ADH90665 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 598  
ID ADJ54704 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 599  
ID ADJ98540 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 600  
ID ADJ98710 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 601  
ID ADH78869 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 602  
ID ADJ99103 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 603  
ID AD099273 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 604  
ID AD098891 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 605  
ID AD079039 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 606  
ID ADK00899 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 607  
ID ADK14420 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 608  
ID ADK82840 standard; protein; 234 AA.  
DE Human PRO polypeptide #31.  
PN US2004043927-A1.  
PD 04-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 609  
ID AD064475 standard; protein; 234 AA.  
DE Human PRO polypeptide #33.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 610  
ID ADM31371 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 611  
ID ADM36418 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.

PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 612  
ID ADM40223 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 613  
ID ADM80869 standard; protein; 234 AA.  
DE Human PRO polypeptide #7.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 614  
ID ADL91873 standard; protein; 234 AA.  
DE Human PRO1864 protein SEQ ID NO:94.  
PN WO2004024076-A2.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 615  
ID ADN37831 standard; protein; 234 AA.  
DE Novel human secreted and transmembrane protein PRO1864.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 8; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 616  
ID ADY18016 standard; protein; 234 AA.  
DE PRO polypeptide SEQ ID NO 3822.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 9; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 617  
ID ADY19397 standard; protein; 234 AA.  
DE PRO polypeptide SEQ ID NO 5203.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1195; DB 9; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 618  
ID ADY77709 standard; protein; 234 AA.  
DE Neoplastic disease detection protein PRO1864.  
PN US2005059102-A1.  
PD 17-MAR-2005.  
PA (EATO//) EATON D L.  
PA (FLIV//) FILVAROFF E.  
PA (GERR//) GERRITSEN M E.  
PA (GODO//) GODDARD A.  
PA (GODO//) GODOWSKI P J.  
PA (GRIM//) GRIMALDI J C.  
PA (GURN//) GURNEY A L.  
PA (WATA//) WATANABE C K.  
PA (WOOD//) WOOD W I.  
Query Match 100.0%; Score 1195; DB 9; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 619  
ID AEA08359 standard; protein; 234 AA.  
DE Steroidogenic acute regulatory protein related (MLN64).  
PN WO2005047536-A2.

PD 26-MAY-2005.  
PA (NOVS ) NOVARTIS AG.  
Query Match 100.0%; Score 1195; DB 9; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-131;  
RESULT 620  
ID AAM41716 standard; protein; 238 AA.  
DE Human polypeptide SEQ ID NO 6647.  
PN WO20015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 100.0%; Score 1195; DB 4; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.6e-131;  
RESULT 621  
ID AAM41715 standard; protein; 238 AA.  
DE Human polypeptide SEQ ID NO 6646.  
PN WO20015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 100.0%; Score 1195; DB 4; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.6e-131;  
RESULT 622  
ID ABB7508 standard; protein; 238 AA.  
DE Human secretory polypeptide SPTM SEQ ID NO 692.  
PN WO200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 100.0%; Score 1195; DB 6; Length 238;  
Best Local Similarity 100.0%; Pred. No. 1.6e-131;  
RESULT 623  
ID ABR58404 standard; protein; 234 AA.  
DE Human NOV19b.  
PN WO2003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 99.4%; Score 1188; DB 6; Length 234;  
Best Local Similarity 99.6%; Pred. No. 1e-130;  
RESULT 624  
ID AAM39930 standard; protein; 216 AA.  
DE Human polypeptide SEQ ID NO 3075.  
PN WO20015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 91.8%; Score 1097; DB 4; Length 216;  
Best Local Similarity 92.3%; Pred. No. 4.7e-120;  
RESULT 625  
ID ABB90287 standard; protein; 201 AA.  
DE Human polypeptide SEQ ID NO 2663.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 85.7%; Score 1024; DB 5; Length 201;  
Best Local Similarity 100.0%; Pred. No. 1.6e-111;  
RESULT 626  
ID ABR58403 standard; protein; 198 AA.  
DE Human NOV19a.  
PN WO2003029423-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 82.4%; Score 985; DB 6; Length 198;  
Best Local Similarity 84.6%; Pred. No. 6.2e-107;  
RESULT 627  
ID AAM0250 standard; protein; 283 AA.  
DE Novel human secreted protein #741.  
PN WO200179449-A2.  
PD 25-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 65.0%; Score 777; DB 4; Length 283;  
Best Local Similarity 72.5%; Pred. No. 3e-82;  
RESULT 628  
ID ABB6413 standard; protein; 176 AA.  
DE Human protein encoded by clone FEBRA20007820.  
PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INSTR.  
Query Match 56.0%; Score 669.5; DB 7; Length 176;  
Best Local Similarity 87.5%; Pred. No. 6.9e-70;  
RESULT 629  
ID ADK36828 standard; protein; 146 AA.  
DE Novel human polypeptide SeqID8910.  
PN WO200216439-A2.  
PD 28-FEB-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 55.6%; Score 665; DB 5; Length 146;  
Best Local Similarity 91.0%; Pred. No. 1.8e-69;  
RESULT 630  
ID ADZ88813 standard; protein; 383 AA.  
DE Breast specific protein SEQ ID NO 180.  
PN WO2005044075-A2.  
PD 19-MAY-2005.  
PA (DIAD-) DIADEXUS INC.  
Query Match 55.6%; Score 664; DB 9; Length 383;  
Best Local Similarity 56.2%; Pred. No. 9e-69;  
RESULT 631  
ID AAM25768 standard; protein; 445 AA.  
DE Human MLN 64.  
PN WO9706256-A2.  
PD 20-FEB-1997.  
PA (INRM ) INST NAT SANTE & RECH MEDICALE.  
PA (CNRS ) CENT NAT RECH SCT.  
PA (UTPA-) UNIV PASTEUR LOUIS.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 55.6%; Score 664; DB 2; Length 445;  
Best Local Similarity 56.2%; Pred. No. 1.1e-68;  
RESULT 632  
ID ABR47530 standard; protein; 445 AA.  
DE Breast cancer associated protein sequence SEQ ID NO.296.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 55.6%; Score 664; DB 6; Length 445;  
Best Local Similarity 56.2%; Pred. No. 1.1e-68;  
RESULT 633  
ID ADH13184 standard; protein; 445 AA.  
DE Human malignant neoplasia-related protein SeqID33.  
PN EPI365034-A2.  
PD 26-NOV-2003.  
PA (FARB ) BAYER AG.  
Query Match 55.6%; Score 664; DB 8; Length 445;  
Best Local Similarity 56.2%; Pred. No. 1.1e-68;  
RESULT 634  
ID AEAL5071 standard; protein; 445 AA.  
DE Human polypeptide #7.  
PN WO2005047534-A2.  
PD 26-MAY-2005.  
PA (FARB ) BAYER HEALTHCARE AG.  
Query Match 55.6%; Score 664; DB 9; Length 445;  
Best Local Similarity 56.2%; Pred. No. 1.1e-68;  
RESULT 635  
ID ADZ88812 standard; protein; 497 AA.  
DE Breast specific protein SEQ ID NO 179.  
PN WO2005044075-A2.  
PD 19-MAY-2005.  
PA (DIAD-) DIADEXUS INC.  
Query Match 55.6%; Score 664; DB 9; Length 497;  
Best Local Similarity 56.2%; Pred. No. 1.3e-68;  
RESULT 636  
ID ABB05498 standard; protein; 534 AA.  
DE Novel human diagnostic protein #5489.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 52.3%; Score 625; DB 4; Length 534;  
Best Local Similarity 48.9%; Pred. No. 5.5e-64;  
RESULT 637

ID ABR69622 standard; protein; 412 AA.  
DE Human CGD-22 protein.  
PN WO2003027263-A2.  
PD 03-APR-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 48.4%; Score 578; DB 6; Length 412;  
Best Local Similarity 58.3%; Pred. No. 1.3e-56;  
RESULT 638  
ID ABR75900 standard; protein; 111 AA.  
DE Human secretory polypeptide SPTM SEQ ID NO 1084.  
PN WO200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 33.9%; Score 405.5; DB 6; Length 111;  
Best Local Similarity 73.7%; Pred. No. 4.1e-39;  
RESULT 639  
ID ABR59968 standard; protein; 580 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 6636.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 28.7%; Score 343; DB 4; Length 580;  
Best Local Similarity 37.8%; Pred. No. 9.2e-31;  
RESULT 640  
ID AAM90384 standard; protein; 70 AA.  
DE Human immune/haematopoietic antigen SEQ ID NO:17977.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 26.9%; Score 322; DB 4; Length 70;  
Best Local Similarity 98.4%; Pred. No. 1.5e-25;  
RESULT 641  
ID AAB96837 standard; protein; 424 AA.  
DE Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.  
PN FR2792651-A1.  
PD 27-OCT-2000.  
PA (CNRS-) CNRS CENT NAT RECH SCI.  
Query Match 7.8%; Score 93.5; DB 4; Length 424;  
Best Local Similarity 21.9%; Pred. No. 0.13;  
RESULT 642  
ID AAU03699 standard; protein; 373 AA.  
DE Group B Streptococcus antigenic protein, ID-176.  
PN WO200332882-A2.  
PD 10-MAY-2001.  
PA (MICR-) MICROBIAL TECHNICS LTD.  
Query Match 7.6%; Score 91; DB 4; Length 373;  
Best Local Similarity 25.7%; Pred. No. 0.22;  
RESULT 643  
ID ADV89705 standard; protein; 605 AA.  
DE Streptococcus agalactiae protein sequence, SEQ ID 2099.  
PN FR2824074-A1.  
PD 31-OCT-2002.  
PA (INSP-) INST PASTEUR.  
Query Match 7.6%; Score 91; DB 8; Length 605;  
Best Local Similarity 25.7%; Pred. No. 0.43;  
RESULT 644  
ID ADV80958 standard; protein; 605 AA.  
DE Streptococcus agalactiae protein, SEQ ID 2099.  
PN WO200292818-A2.  
PD 21-NOV-2002.  
PA (INSP-) INST PASTEUR.  
Query Match 7.6%; Score 91; DB 8; Length 605;  
Best Local Similarity 25.7%; Pred. No. 0.43;  
RESULT 645  
ID ABR30317 standard; protein; 651 AA.  
DE Streptococcus polypeptide SEQ ID NO 9810.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 7.6%; Score 91; DB 8; Length 651;  
Best Local Similarity 25.7%; Pred. No. 0.48;  
RESULT 646  
ID ADV83104 standard; protein; 651 AA.  
DE Streptococcus agalactiae protein, SEQ ID 4245.  
PN WO200292818-A2.  
PD 21-NOV-2002.  
PA (INSP-) INST PASTEUR.  
Query Match 7.6%; Score 91; DB 8; Length 651;  
Best Local Similarity 25.7%; Pred. No. 0.48;  
RESULT 647  
ID ABR29732 standard; protein; 654 AA.  
DE Streptococcus polypeptide SEQ ID NO 8640.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 7.6%; Score 91; DB 5; Length 654;  
Best Local Similarity 25.7%; Pred. No. 0.48;  
RESULT 648  
ID ABR26469 standard; protein; 654 AA.  
DE Streptococcus polypeptide SEQ ID NO 2114.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 7.6%; Score 91; DB 5; Length 654;  
Best Local Similarity 25.7%; Pred. No. 0.48;  
RESULT 649  
ID AAG61678 standard; protein; 155 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80037.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.3%; Score 87.5; DB 3; Length 155;  
Best Local Similarity 21.4%; Pred. No. 0.17;  
RESULT 650  
ID AAG59938 standard; protein; 155 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77441.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.3%; Score 87.5; DB 3; Length 155;  
Best Local Similarity 21.4%; Pred. No. 0.17;  
RESULT 651  
ID AAB58945 standard; protein; 516 AA.  
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 653.  
PN WO200055173-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 7.3%; Score 87.5; DB 3; Length 516;  
Best Local Similarity 25.2%; Pred. No. 0.9;  
RESULT 652  
ID ADQ39266 standard; protein; 421 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 929.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.3%; Score 87; DB 8; Length 421;  
Best Local Similarity 23.7%; Pred. No. 0.77;  
RESULT 653  
ID ADQ39263 standard; protein; 223 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 926.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 223;  
Best Local Similarity 25.5%; Pred. No. 0.48;  
RESULT 654  
ID ADQ39258 standard; protein; 285 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 921.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.

Query Match 7.2%; Score 85.5; DB 8; Length 285;  
Best Local Similarity 25.5%; Pred. No. 0.68;  
RESULT 655  
ID ADQ39262 standard; protein; 315 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 925.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 315;  
Best Local Similarity 25.5%; Pred. No. 0.78;  
RESULT 656  
ID ADQ39260 standard; protein; 323 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 923.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 323;  
Best Local Similarity 25.5%; Pred. No. 0.8;  
RESULT 657  
ID ADQ39261 standard; protein; 328 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 924.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 328;  
Best Local Similarity 25.5%; Pred. No. 0.82;  
RESULT 658  
ID ADQ39265 standard; protein; 338 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 928.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 338;  
Best Local Similarity 25.5%; Pred. No. 0.86;  
RESULT 659  
ID ADQ39267 standard; protein; 339 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 930.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 339;  
Best Local Similarity 25.5%; Pred. No. 0.86;  
RESULT 660  
ID ADE28099 standard; protein; 340 AA.  
DE Human NTPAN protein - SEQ ID 4.  
PN WO2003051902-A1.  
PD 26-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.2%; Score 85.5; DB 7; Length 340;  
Best Local Similarity 25.5%; Pred. No. 0.86;  
RESULT 661  
ID ADQ39269 standard; protein; 384 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 932.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 384;  
Best Local Similarity 25.5%; Pred. No. 1;  
RESULT 662  
ID ADQ39264 standard; protein; 390 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 927.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 390;  
Best Local Similarity 25.5%; Pred. No. 1;  
RESULT 663  
ID ABU26680 standard; protein; 396 AA.  
DE Protein encoded by Prokaryotic essential gene #12207.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 7.2%; Score 85.5; DB 6; Length 396;

Best Local Similarity 21.0%; Pred. No. 1.1;  
RESULT 664  
ID AAM13575 standard; protein; 438 AA.  
DE Batten disease polypeptide CLN3.  
PN WO9708308-A1.  
PD 06-MAR-1997.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 7.2%; Score 85.5; DB 2; Length 438;  
Best Local Similarity 25.5%; Pred. No. 1.2;  
RESULT 665  
ID AAM13589 standard; protein; 438 AA.  
DE Batten disease CLN3 mutant protein in family L204.  
PN WO9708308-A1.  
PD 06-MAR-1997.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 7.2%; Score 85.5; DB 2; Length 438;  
Best Local Similarity 24.8%; Pred. No. 1.2;  
RESULT 666  
ID AAM13582 standard; protein; 438 AA.  
DE Batten disease CLN3 mutant protein in family L46.  
PN WO9708308-A1.  
PD 06-MAR-1997.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 7.2%; Score 85.5; DB 2; Length 438;  
Best Local Similarity 25.5%; Pred. No. 1.2;  
RESULT 667  
ID AAM13577 standard; protein; 438 AA.  
DE Batten disease CLN3 mutant protein in family L39.  
PN WO9708308-A1.  
PD 06-MAR-1997.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 7.2%; Score 85.5; DB 2; Length 438;  
Best Local Similarity 25.5%; Pred. No. 1.2;  
RESULT 668  
ID ADQ6392 standard; protein; 438 AA.  
DE T cell activation associated protein #285.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 438;  
Best Local Similarity 25.5%; Pred. No. 1.2;  
RESULT 669  
ID ADQ39268 standard; protein; 438 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 931.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 7.2%; Score 85.5; DB 8; Length 438;  
Best Local Similarity 25.5%; Pred. No. 1.2;  
RESULT 670  
ID ADA05822 standard; protein; 440 AA.  
DE Human NOV43a protein SEQ ID NO:182.  
PN WO2003029424-A2.  
PD 10-APR-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.2%; Score 85.5; DB 6; Length 440;  
Best Local Similarity 25.2%; Pred. No. 1.2;  
RESULT 671  
ID ADN63244 standard; protein; 440 AA.  
DE Human NOV43a variant.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLET I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUT/) JU J.  
PA (LILL/) LI L.  
PA (GUOX/) GUO X.



PA (PATY/) PATTRAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERR/) ZERRHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIMW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIP1/) DIP1PO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match  
Best Local Similarity 7.2%; Score 85.5; DB 8; Length 440;  
RESULT 672  
ID AD62985 standard; protein; 440 AA.  
DE Human NOV43a.  
PN US2004038223-A1.  
PD 26-FEB-2004.  
PA (SMIT/) SMITHSON G.  
PA (MILL/) MILLER I.  
PA (PEYM/) PEYMAN J A.  
PA (KEKU/) KEKUDA R.  
PA (JUJU/) JU J.  
PA (LILU/) LI L.  
PA (GUOX/) GUO X.  
PA (PATY/) PATTRAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (EDIN/) EDINGER S R.  
PA (ELLE/) ELLERMAN K.  
PA (MALY/) MALYANKAR U M.  
PA (ORTT/) ORT T.  
PA (GORM/) GORMAN L.  
PA (ZERR/) ZERRHUSEN B D.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (CATT/) CATTERTON E.  
PA (JIMW/) JI W.  
PA (MILL/) MILLER C E.  
PA (RAST/) RASTELLI L.  
PA (STON/) STONE D J.  
PA (PENA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (SHIM/) SHIMKETS R A.  
PA (ROTH/) ROTHENBERG M E.  
PA (LEAC/) LEACH M D.  
PA (AGEE/) AGEE M L.  
PA (BERG/) BERGHS C.  
PA (DIP1/) DIP1PO V A.  
PA (EISE/) EISEN A.  
PA (GANG/) GANGOLLI E A.  
PA (RIEG/) RIEGER D K.  
PA (SPAD/) SPADERNA S K.  
Query Match  
Best Local Similarity 7.2%; Score 85.5; DB 8; Length 440;  
RESULT 673  
ID AAM13593 standard; protein; 467 AA.  
DE Batten disease CLN3 mutant protein in family L61.

PN W09708308-A1.  
PD 06-MAR-1997.  
PA (GEHO/) GEN HOSPITAL CORP.  
PA (UYLE-) RUCKSUNIV LEIDEN.  
Query Match  
Best Local Similarity 7.2%; Score 85.5; DB 2; Length 467;  
RESULT 674  
ID ABB89640 standard; protein; 473 AA.  
DE Human polypeptide SEQ ID NO 2016.  
PN W0200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 7.2%; Score 85.5; DB 5; Length 473;  
RESULT 675  
ID ADQ18055 standard; protein; 473 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 872.  
PN W02004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 7.2%; Score 85.5; DB 8; Length 473;  
RESULT 676  
ID ADU06406 standard; protein; 473 AA.  
DE Novel bronchial cancer-associated human protein SeqID630.  
PN DE10316701-A1.  
PD 04-NOV-2004.  
PA (HINZ/) HINZMANN B.  
PA (HERM/) HERMANN K.  
PA (CAST/) HEIDEN CASTRANOS-VELEZ E.  
Query Match  
Best Local Similarity 7.2%; Score 85.5; DB 8; Length 473;  
RESULT 677  
ID ADY20253 standard; protein; 473 AA.  
DE PRO polypeptide SEQ ID NO 6059.  
PN W02005016962-A2.  
PD 24-FEB-2005.  
PA (GERTH/) GENENTECH INC.  
Query Match  
Best Local Similarity 7.2%; Score 85.5; DB 9; Length 473;  
RESULT 678  
ID ABU40544 standard; protein; 500 AA.  
DE Plant full length insert polypeptide seqid 65247.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match  
Best Local Similarity 7.1%; Score 85; DB 8; Length 527;  
RESULT 679  
ID ADY09432 standard; protein; 527 AA.  
DE Plant full length insert polypeptide seqid 65247.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match  
Best Local Similarity 7.1%; Score 85; DB 8; Length 527;  
RESULT 680  
ID ABU33210 standard; protein; 430 AA.  
DE Protein encoded by Prokaryotic essential gene #18737.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 7.1%; Score 84.5; DB 6; Length 430;  
RESULT 681  
ID AAM13588 standard; protein; 438 AA.  
DE Batten disease CLN3 mutant protein in family L10.  
PN W09708308-A1.

PD 06-MAR-1997.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 7.1%; Score 84.5; DB 2; Length 438;  
Best Local Similarity 24.8%; Pred. No. 1.6;  
RESULT 682  
ID AAG16921 standard; protein; 322 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17749.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 7.0%; Score 83.5; DB 3; Length 322;  
Best Local Similarity 33.7%; Pred. No. 1.4;  
RESULT 683  
ID ABG21285 standard; protein; 472 AA.  
DE Novel human diagnostic protein #1276.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.0%; Score 83.5; DB 4; Length 472;  
Best Local Similarity 20.1%; Pred. No. 2.3;  
RESULT 684  
ID AB035608 standard; protein; 239 AA.  
DE Protein encoded by prokaryotic essential gene #21135.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.9%; Score 82.5; DB 6; Length 239;  
Best Local Similarity 21.7%; Pred. No. 1.2;  
RESULT 685  
ID ADU25550 standard; protein; 389 AA.  
DE L. acidophilus cell surface protein homologue #63.  
PN WO2004096992-A2.  
PD 11-NOV-2004.  
PA (UYNC-) UNIV NORTH CAROLINA STATE.  
Query Match 6.9%; Score 82.5; DB 8; Length 389;  
Best Local Similarity 24.7%; Pred. No. 2.3;  
RESULT 686  
ID AAM13590 standard; protein; 438 AA.  
DE Batten disease CLN3 mutant protein in family L216.  
PN WO9708308-A1.  
PD 06-MAR-1997.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 6.9%; Score 82.5; DB 2; Length 438;  
Best Local Similarity 24.8%; Pred. No. 2.8;  
RESULT 687  
ID ADB85263 standard; protein; 589 AA.  
DE Mouse RNA1 homologue SEQ ID NO:144.  
PN EP1284297-A2.  
PD 19-FEB-2003.  
PA (WARN ) WARNER LAMBERT CO.  
Query Match 6.9%; Score 82; DB 7; Length 589;  
Best Local Similarity 19.5%; Pred. No. 4.8;  
RESULT 688  
ID ADX74800 standard; protein; 264 AA.  
DE Plant full length insert polypeptide seqid 44166.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LITU/) LITU J.  
PA (ZHOV/) ZHOV Y.  
PA (KHOV/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABR/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 6.8%; Score 81.5; DB 8; Length 264;  
Best Local Similarity 33.3%; Pred. No. 1.8;  
RESULT 689  
ID AAM13586 standard; protein; 438 AA.  
DE Batten disease CLN3 mutant protein in family L285.  
PN WO9708308-A1.  
PD 06-MAR-1997.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 6.8%; Score 81.5; DB 2; Length 438;  
Best Local Similarity 24.8%; Pred. No. 3.6;  
RESULT 690  
ID AAB92924 standard; protein; 519 AA.  
DE Human protein sequence SEQ ID NO:11574.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 6.8%; Score 81.5; DB 4; Length 519;  
Best Local Similarity 22.6%; Pred. No. 4.6;  
RESULT 691  
ID ADE28193 standard; protein; 577 AA.  
DE Human MBDT protein - SEQ ID 43.  
PN WO2003046152-A2.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.8%; Score 81.5; DB 7; Length 577;  
Best Local Similarity 22.6%; Pred. No. 5.3;  
RESULT 692  
ID ADN23155 standard; protein; 529 AA.  
DE Bacterial polypeptide #5808.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.8%; Score 81; DB 8; Length 529;  
Best Local Similarity 23.1%; Pred. No. 5.4;  
RESULT 693  
ID ADN23156 standard; protein; 529 AA.  
DE Bacterial polypeptide #5809.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.8%; Score 81; DB 8; Length 529;  
Best Local Similarity 23.1%; Pred. No. 5.4;  
RESULT 694  
ID AAG53771 standard; protein; 322 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68491.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.7%; Score 80.5; DB 3; Length 322;  
Best Local Similarity 32.7%; Pred. No. 3.1;  
RESULT 695  
ID AAG25639 standard; protein; 322 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29783.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.7%; Score 80.5; DB 3; Length 322;  
Best Local Similarity 32.7%; Pred. No. 3.1;  
RESULT 696  
ID AAG53746 standard; protein; 322 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68457.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.7%; Score 80.5; DB 3; Length 322;  
Best Local Similarity 32.7%; Pred. No. 3.1;  
RESULT 697  
ID ABO63194 standard; protein; 350 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9711.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.7%; Score 80.5; DB 7; Length 350;  
Best Local Similarity 31.8%; Pred. No. 3.5;  
RESULT 698  
ID ABB48552 standard; protein; 463 AA.

DE Listeria monocytogenes protein #1256.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP ) INST PASTEUR.  
Query Match 6.7%; Score 80.5; DB 5; Length 463;  
Best Local Similarity 19.0%; Pred. No. 5.1;  
RESULT 699  
ID ABU31306 standard; protein; 463 AA.  
DE Protein encoded by Prokaryotic essential gene #18563.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.7%; Score 80.5; DB 6; Length 463;  
Best Local Similarity 19.0%; Pred. No. 5.1;  
RESULT 700  
ID ADD43870 standard; protein; 536 AA.  
DE Chlamydia trachomatis immunogenic protein, SEQ ID NO 165.  
PN WO2003049762-A2.  
PD 19-JUN-2003.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.7%; Score 80.5; DB 7; Length 536;  
Best Local Similarity 25.2%; Pred. No. 6.3;  
RESULT 701  
ID AEA19162 standard; protein; 536 AA.  
DE Chlamydia trachomatis protein - SEQ ID 165.  
PN US2005106162-A1.  
PD 19-MAY-2005.  
PA (GRAN/) GRANDI G.  
PA (RAT/) RATTI G.  
Query Match 6.7%; Score 80.5; DB 9; Length 536;  
Best Local Similarity 25.2%; Pred. No. 6.3;  
RESULT 702  
ID ADC42920 standard; protein; 891 AA.  
DE Vaccinia Virus Major Core Protein P4a precursor.  
PN WO2003017943-A2.  
PD 06-MAR-2003.  
PA (MYRI-) MYRIAD GENETICS INC.  
Query Match 6.7%; Score 80.5; DB 7; Length 891;  
Best Local Similarity 23.3%; Pred. No. 13;  
RESULT 703  
ID ABB92830 standard; protein; 1780 AA.  
DE Hebbicidally active polypeptide SEQ ID NO 2041.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB ) BAYER AG.  
Query Match 6.7%; Score 80.5; DB 5; Length 1780;  
Best Local Similarity 20.8%; Pred. No. 33;  
RESULT 704  
ID AAB54399 standard; protein; 144 AA.  
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:851.  
PN WO2000055320-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.7%; Score 80; DB 3; Length 144;  
Best Local Similarity 25.4%; Pred. No. 1.2;  
RESULT 705  
ID AAM39952 standard; protein; 238 AA.  
DE Human polypeptide SEQ ID NO 3097.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.7%; Score 80; DB 4; Length 238;  
Best Local Similarity 22.5%; Pred. No. 2.3;  
RESULT 706  
ID ADM04473 standard; protein; 238 AA.  
DE Human protein of the invention SEQ ID NO:3158.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.7%; Score 80; DB 7; Length 238;  
Best Local Similarity 22.5%; Pred. No. 2.3;  
RESULT 707  
ID AAM41738 standard; protein; 249 AA.

DE Human polypeptide SEQ ID NO 6669.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.7%; Score 80; DB 4; Length 249;  
Best Local Similarity 22.5%; Pred. No. 2.5;  
RESULT 708  
ID AAK77844 standard; protein; 309 AA.  
DE Molasses toxicity resistance protein RTM1.  
PN WO9514774-A2.  
PD 01-JUN-1995.  
PA (CNRS ) CENT NAT RECH SCI.  
Query Match 6.7%; Score 80; DB 2; Length 309;  
Best Local Similarity 28.0%; Pred. No. 3.4;  
RESULT 709  
ID AAM67388 standard; protein; 330 AA.  
DE Photorhabdus luminescens protein sequence #485.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.7%; Score 80; DB 6; Length 330;  
Best Local Similarity 24.6%; Pred. No. 3.7;  
RESULT 710  
ID AAB03831 standard; protein; 360 AA.  
DE Human gene 14 encoded secreted protein HDGFN31, SEQ ID NO: 77.  
PN WO200136440-A1.  
PD 25-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.7%; Score 80; DB 4; Length 360;  
Best Local Similarity 22.5%; Pred. No. 4.1;  
RESULT 711  
ID AAB64559 standard; protein; 360 AA.  
DE Human albumin fusion protein #1234.  
PN WO20017137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.7%; Score 80; DB 5; Length 360;  
Best Local Similarity 22.5%; Pred. No. 4.1;  
RESULT 712  
ID ADL77826 standard; protein; 360 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1308.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 6.7%; Score 80; DB 8; Length 360;  
Best Local Similarity 22.5%; Pred. No. 4.1;  
RESULT 713  
ID ADX66260 standard; protein; 516 AA.  
DE Plant full length insert polypeptide seqid 37103.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 6.7%; Score 80; DB 8; Length 516;  
Best Local Similarity 20.0%; Pred. No. 6.8;  
RESULT 714  
ID ABU25554 standard; protein; 365 AA.  
DE Protein encoded by Prokaryotic essential gene #11081.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.7%; Score 79.5; DB 6; Length 365;  
Best Local Similarity 21.2%; Pred. No. 4.8;  
RESULT 715  
ID AAR58703 standard; protein; 406 AA.  
DE HCMV IE-exon-4 subunit.  
PN WO9417810-A1.

PD 18-AUG-1994.  
PA (MIST-) MISTAR INST ANATOMY & BIOLOGY.  
Query Match 6.7%; Score 79.5; DB 2; Length 406;  
Best Local Similarity 19.3%; Pred. No. 5.6;  
RESULT 716  
ID AAM27275 standard; protein; 406 AA.  
DE Human cytomagalovirus immediate-early exon 4 product.  
PN W09740165-A1.  
PD 30-OCT-1997.  
PA (MIST-) MISTAR INST ANATOMY & BIOLOGY.  
Query Match 6.7%; Score 79.5; DB 2; Length 406;  
Best Local Similarity 19.3%; Pred. No. 5.6;  
RESULT 717  
ID ABB58483 standard; protein; 638 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2241.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 6.7%; Score 79.5; DB 4; Length 638;  
Best Local Similarity 20.5%; Pred. No. 10;  
RESULT 718  
ID AAE13277 standard; protein; 723 AA.  
DE Human transporters and ion channels (TRICH)-4.  
PN W0200177174-A2.  
PD 18-OCT-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.7%; Score 79.5; DB 5; Length 723;  
Best Local Similarity 18.0%; Pred. No. 12;  
RESULT 719  
ID ADL12774 standard; protein; 723 AA.  
DE Human steroid-induced C3A liver cell protein #80.  
PN US6673549-B1.  
PD 06-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.7%; Score 79.5; DB 8; Length 723;  
Best Local Similarity 18.0%; Pred. No. 12;  
RESULT 720  
ID AAM20696 standard; protein; 121 AA.  
DE H. pylori secreted or periplasmic protein 05ae20220orf50.  
PN W09640893-A1.  
PD 19-DEC-1996.  
PA (ASTR ) ASTRA AB.  
Query Match 6.6%; Score 79; DB 2; Length 121;  
Best Local Similarity 21.4%; Pred. No. 1.2;  
RESULT 721  
ID ABB60462 standard; protein; 323 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 8178.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 6.6%; Score 79; DB 4; Length 323;  
Best Local Similarity 18.8%; Pred. No. 4.7;  
RESULT 722  
ID AEB41478 standard; protein; 356 AA.  
DE L. pneumophila protein SEQ ID NO 5810.  
PN W02005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.6%; Score 79; DB 9; Length 356;  
Best Local Similarity 23.0%; Pred. No. 5.4;  
RESULT 723  
ID AEB38189 standard; protein; 358 AA.  
DE L. pneumophila protein SEQ ID NO 2521.  
PN W02005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.6%; Score 79; DB 9; Length 358;

Best Local Similarity 23.0%; Pred. No. 5.4;  
RESULT 724  
ID ABR58610 standard; protein; 1531 AA.  
DE Human cancer related protein SEQ ID NO:267.  
PN W02003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.6%; Score 79; DB 6; Length 1531;  
Best Local Similarity 24.3%; Pred. No. 40;  
RESULT 725  
ID ADE31753 standard; protein; 1531 AA.  
DE Human 59590 protein #SEQ ID 110.  
PN W02003065984-A2.  
PD 14-AUG-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.6%; Score 79; DB 7; Length 1531;  
Best Local Similarity 24.3%; Pred. No. 40;  
RESULT 726  
ID ABU62069 standard; protein; 1597 AA.  
DE Human heart alpha-kinase (HK).  
PN US2002177205-A1.  
PD 28-NOV-2002.  
PA (RYAZ/) RYAZANOV A.  
Query Match 6.6%; Score 79; DB 6; Length 1597;  
Best Local Similarity 24.3%; Pred. No. 43;  
RESULT 727  
ID ABU62070 standard; protein; 1597 AA.  
DE Mouse heart alpha-kinase (HK).  
PN US2002177205-A1.  
PD 28-NOV-2002.  
PA (RYAZ/) RYAZANOV A.  
Query Match 6.6%; Score 79; DB 6; Length 1597;  
Best Local Similarity 24.3%; Pred. No. 43;  
RESULT 728  
ID ABO35689 standard; protein; 135 AA.  
DE Human genome derived single exon protein #1923.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 6.6%; Score 79; DB 8; Length 135;  
Best Local Similarity 59.4%; Pred. No. 1.6;  
RESULT 729  
ID ADU02890 standard; protein; 165 AA.  
DE Novel human polypeptide seqid 1357.  
PN W02004093804-A2.  
PD 04-NOV-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 6.6%; Score 78.5; DB 8; Length 165;  
Best Local Similarity 24.6%; Pred. No. 2.1;  
RESULT 730  
ID AEB38367 standard; protein; 205 AA.  
DE L. pneumophila protein SEQ ID NO 2699.  
PN W02005049642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.6%; Score 78.5; DB 9; Length 205;  
Best Local Similarity 18.3%; Pred. No. 2.9;  
RESULT 731  
ID ADB10816 standard; protein; 228 AA.  
DE Alloiococcus ocellis antigenic protein SEQ ID NO:4244.  
PN W02003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP ) WYETH HOLDINGS CORP.  
Query Match 6.6%; Score 78.5; DB 6; Length 228;  
Best Local Similarity 22.5%; Pred. No. 3.3;  
RESULT 732  
ID ABU36298 standard; protein; 239 AA.  
DE Protein encoded by Prokaryotic essential gene #21825.

PN WO200277183-A2.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.6%; Score 78.5; DB 6; Length 239;  
Best Local Similarity 23.4%; Pred. No. 3.5;  
RESULT 733  
ID ADJ27174 standard; protein; 626 AA.  
DE Human TRICH-6, SEQ ID 6.  
PN WO2004013293-A2.  
PD 12-FEB-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.6%; Score 78.5; DB 8; Length 626;  
Best Local Similarity 18.0%; Pred. No. 13;  
RESULT 734  
ID ABM84879 standard; protein; 648 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5128.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.6%; Score 78.5; DB 8; Length 648;  
Best Local Similarity 18.0%; Pred. No. 14;  
RESULT 735  
ID ABM84877 standard; protein; 668 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5126.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.6%; Score 78.5; DB 8; Length 668;  
Best Local Similarity 18.0%; Pred. No. 15;  
RESULT 736  
ID ABP29904 standard; protein; 669 AA.  
DE Streptococcus polypeptide SEQ ID NO 8984.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 6.6%; Score 78.5; DB 5; Length 669;  
Best Local Similarity 23.5%; Pred. No. 15;  
RESULT 737  
ID ABP28724 standard; protein; 669 AA.  
DE Streptococcus polypeptide SEQ ID NO 6624.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 6.6%; Score 78.5; DB 5; Length 669;  
Best Local Similarity 23.5%; Pred. No. 15;  
RESULT 738  
ID ADI21047 standard; protein; 703 AA.  
DE Novel human protein #22.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.6%; Score 78.5; DB 7; Length 703;  
Best Local Similarity 18.0%; Pred. No. 16;  
RESULT 739  
ID ABM84882 standard; protein; 711 AA.  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5131.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.6%; Score 78.5; DB 8; Length 711;  
Best Local Similarity 18.0%; Pred. No. 16;  
RESULT 740  
ID ABP52105 standard; protein; 723 AA.  
DE Home sapiens ABC transporter ABCB9 protein SEQ ID NO:57.  
PN EP117066-A1.  
PD 26-JUN-2002.  
PA (UYGE-) UNIV GENT.  
Query Match 6.6%; Score 78.5; DB 5; Length 723;  
Best Local Similarity 18.0%; Pred. No. 16;  
RESULT 741  
ID ADQ97094 standard; protein; 723 AA.

DE Human cancer associated sequence HPL-10-005, SEQ ID 70.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 6.6%; Score 78.5; DB 8; Length 723;  
Best Local Similarity 18.0%; Pred. No. 16;  
RESULT 742  
ID AAE02437 standard; protein; 766 AA.  
DE Human ATP binding cassette, ABCB9 transporter protein.  
PN WO200140305-A1.  
PD 07-JUN-2001.  
PA (ACTI-) ACTIVE PASS PHARM INC.  
Query Match 6.6%; Score 78.5; DB 4; Length 766;  
Best Local Similarity 18.0%; Pred. No. 18;  
RESULT 743  
ID AAE02441 standard; protein; 766 AA.  
DE Human ATP binding cassette, ABCB9 transporter protein mutant K545R.  
PN WO200140305-A1.  
PD 07-JUN-2001.  
PA (ACTI-) ACTIVE PASS PHARM INC.  
Query Match 6.6%; Score 78.5; DB 4; Length 766;  
Best Local Similarity 18.0%; Pred. No. 18;  
RESULT 744  
ID AAE02442 standard; protein; 766 AA.  
DE Human ATP binding cassette, ABCB9 transporter protein mutant D667N.  
PN WO200140305-A1.  
PD 07-JUN-2001.  
PA (ACTI-) ACTIVE PASS PHARM INC.  
Query Match 6.6%; Score 78.5; DB 4; Length 766;  
Best Local Similarity 18.0%; Pred. No. 18;  
RESULT 745  
ID AAG67163 standard; protein; 766 AA.  
DE Amino acid binding sequence of a human 33894 transporter polypeptide.  
PN WO200164875-A2.  
PD 07-SEP-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.6%; Score 78.5; DB 4; Length 766;  
Best Local Similarity 18.0%; Pred. No. 18;  
RESULT 746  
ID AAG79246 standard; protein; 766 AA.  
DE Amino acid sequence of a human TAP-like (HUTAPL) polypeptide.  
PN WO200173018-A2.  
PD 04-OCT-2001.  
PA (MERE-) MERCK PATENT GMBH.  
Query Match 6.6%; Score 78.5; DB 4; Length 766;  
Best Local Similarity 18.0%; Pred. No. 18;  
RESULT 747  
ID ABB98345 standard; protein; 766 AA.  
DE Human ABC transporter ABCB9 SEQ ID NO 6.  
PN WO200264781-A2.  
PD 22-AUG-2002.  
PA (ACTI-) ACTIVE PASS PHARM INC.  
Query Match 6.6%; Score 78.5; DB 5; Length 766;  
Best Local Similarity 18.0%; Pred. No. 18;  
RESULT 748  
ID AAE21170 standard; protein; 766 AA.  
DE Human TRICH-14 protein.  
PN WO200212340-A2.  
PD 14-FEB-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.6%; Score 78.5; DB 5; Length 766;  
Best Local Similarity 18.0%; Pred. No. 18;  
RESULT 749  
ID ADQ97096 standard; protein; 766 AA.  
DE Human cancer associated sequence HP2-10-005, SEQ ID 72.  
PN WO2004060304-A2.  
PD 22-JUN-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 6.6%; Score 78.5; DB 8; Length 766;  
Best Local Similarity 18.0%; Pred. No. 18;  
RESULT 750  
ID AAG20805 standard; protein; 377 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23131.

PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 6.5%; Score 78; DB 3; Length 377;  
Best Local Similarity 23.8%; Pred. No. 7.6;  
RESULT 751  
ID AAG20804 standard; protein; 442 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23130.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 6.5%; Score 78; DB 3; Length 442;  
Best Local Similarity 23.8%; Pred. No. 9.5;  
RESULT 752  
ID AAV35545 standard; protein; 471 AA.  
DE Haemophilus influenzae cellular proliferation protein #186.  
PN W020017055-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.5%; Score 78; DB 4; Length 471;  
Best Local Similarity 25.0%; Pred. No. 10;  
RESULT 753  
ID AEU30411 standard; protein; 471 AA.  
DE Protein encoded by prokaryotic essential gene #15938.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.5%; Score 78; DB 6; Length 471;  
Best Local Similarity 25.0%; Pred. No. 10;  
RESULT 754  
ID AAG20803 standard; protein; 489 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23129.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 6.5%; Score 78; DB 3; Length 489;  
Best Local Similarity 23.8%; Pred. No. 11;  
RESULT 755  
ID ABB49039 standard; protein; 269 AA.  
DE Listeria monocytogenes protein #1743.  
PN W020017335-A2.  
PD 18-OCT-2001.  
PA (INSP-) INST PASTEUR.  
Query Match 6.5%; Score 77.5; DB 5; Length 269;  
Best Local Similarity 22.0%; Pred. No. 5.4;  
RESULT 756  
ID ABG17374 standard; protein; 280 AA.  
DE Novel human diagnostic protein #17355.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.5%; Score 77.5; DB 4; Length 280;  
Best Local Similarity 21.9%; Pred. No. 5.8;  
RESULT 757  
ID ABO00771 standard; protein; 280 AA.  
DE Polypeptide encoded by novel human config #22.  
PN W02003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.5%; Score 77.5; DB 6; Length 280;  
Best Local Similarity 21.9%; Pred. No. 5.8;  
RESULT 758  
ID ABU4889 standard; protein; 327 AA.  
DE Protein encoded by prokaryotic essential gene #34416.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.5%; Score 77.5; DB 6; Length 327;  
Best Local Similarity 24.8%; Pred. No. 7.1;  
RESULT 759  
ID AAW13576 standard; protein; 438 AA.  
DE Mouse Barten disease polypeptide CLN3 homologue.  
PN W09708308-A1.  
PD 06-MAR-1997.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (UYLE-) RIJCKSUNIV LEIDEN.  
Query Match 6.5%; Score 77; DB 8; Length 490;  
Best Local Similarity 19.5%; Pred. No. 14;  
RESULT 760  
ID ADG42965 standard; protein; 491 AA.  
DE Bacterial polypeptide #21395.  
PN US2003231675-A1.  
PD 18-DEC-2003.  
PA (CAOV-) CAO Y.  
PA (HINK-) HINKLE G J.  
PA (SLAT-) SLATER S C.  
PA (CHEN-) CHEN X.  
PA (GOLD-) GOLDMAN B S.  
Query Match 6.5%; Score 77.5; DB 8; Length 491;  
Best Local Similarity 22.6%; Pred. No. 13;  
RESULT 761  
ID ADC42919 standard; protein; 892 AA.  
DE Variola smallpox virus A10L.  
PN W02003017943-A2.  
PD 06-MAR-2003.  
PA (MYRI-) MYRIAD GENETICS INC.  
Query Match 6.5%; Score 77.5; DB 7; Length 892;  
Best Local Similarity 22.7%; Pred. No. 29;  
RESULT 762  
ID AAR88413 standard; protein; 353 AA.  
DE High-affinity melatonin-1a receptor.  
PN W09535320-A1.  
PD 28-DEC-1995.  
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
Query Match 6.4%; Score 77; DB 2; Length 353;  
Best Local Similarity 22.1%; Pred. No. 9.1;  
RESULT 763  
ID AAW23958 standard; protein; 353 AA.  
DE Mouse melatonin 1a receptor.  
PN W09803549-A1.  
PD 29-JAN-1998.  
PA (GEHO-) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 77; DB 2; Length 353;  
Best Local Similarity 22.1%; Pred. No. 9.1;  
RESULT 764  
ID ABB07571 standard; protein; 353 AA.  
DE Mouse melatonin 1a (Mela) receptor.  
PN US6326526-B1.  
PD 04-DEC-2001.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
PA (GEHO-) GEN HOSPITAL CORP.  
Query Match 6.4%; Score 77; DB 5; Length 353;  
Best Local Similarity 22.1%; Pred. No. 9.1;  
RESULT 765  
ID ADO29553 standard; protein; 353 AA.  
DE Mouse GPCR MTN1A, SEQ ID NO:655.  
PN W02004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 6.4%; Score 77; DB 8; Length 353;  
Best Local Similarity 22.1%; Pred. No. 9.1;  
RESULT 766  
ID ADM25403 standard; protein; 383 AA.  
DE Hyperthermophile Methanopyrus kandleri protein #9.  
PN W02003076575-A2.  
PD 18-SEP-2003.  
PA (FIDE-) FIDELITY SYSTEMS INC.  
PA (MALY-) MALYKH A.  
Query Match 6.4%; Score 77; DB 7; Length 383;  
Best Local Similarity 24.8%; Pred. No. 10;  
RESULT 767  
ID ADQ95948 standard; protein; 490 AA.  
DE T cell activation associated protein #63.  
PN W02004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 6.4%; Score 77; DB 8; Length 490;  
Best Local Similarity 19.5%; Pred. No. 14;  
RESULT 768

ID A0096002 standard; protein; 490 AA.  
DE T cell activation associated protein #90.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match Best Local Similarity 6.4%; Score 77; DB 8; Length 490;  
Pred. No. 14;  
RESULT 769  
ID AAG42521 standard; protein; 648 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53040.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match Best Local Similarity 6.4%; Score 77; DB 3; Length 648;  
Pred. No. 21;  
RESULT 770  
ID ABU16172 standard; protein; 650 AA.  
DE Protein encoded by Prokaryotic essential gene #1699.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match Best Local Similarity 6.4%; Score 77; DB 6; Length 650;  
Pred. No. 21;  
RESULT 771  
ID AEM72713 standard; protein; 650 AA.  
DE Staphylococcus aureus protein #1953.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match Best Local Similarity 6.4%; Score 77; DB 6; Length 650;  
Pred. No. 21;  
RESULT 772  
ID AAG42520 standard; protein; 690 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53039.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match Best Local Similarity 6.4%; Score 77; DB 3; Length 690;  
Pred. No. 23;  
RESULT 773  
ID AAG42519 standard; protein; 728 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53038.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match Best Local Similarity 6.4%; Score 77; DB 3; Length 728;  
Pred. No. 25;  
RESULT 774  
ID AAG32549 standard; protein; 805 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39287.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match Best Local Similarity 6.4%; Score 77; DB 3; Length 805;  
Pred. No. 29;  
RESULT 775  
ID AAG32548 standard; protein; 847 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39286.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match Best Local Similarity 6.4%; Score 77; DB 3; Length 847;  
Pred. No. 31;  
RESULT 776  
ID AAG32547 standard; protein; 991 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39285.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match Best Local Similarity 6.4%; Score 77; DB 3; Length 991;  
Pred. No. 38;  
RESULT 777  
ID ABP52133 standard; protein; 1025 AA.  
DE Plasmodium falciparum multidrug resistance protein SEQ ID NO: 85.  
PN EPI1217066-A1.  
PD 26-JUN-2002.  
PA (UYGE-) UNIV GENT.  
Query Match Best Local Similarity 6.4%; Score 77; DB 5; Length 1025;  
Pred. No. 40;

RESULT 778  
ID AAG42381 standard; protein; 1047 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52849.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match Best Local Similarity 6.4%; Score 77; DB 3; Length 1047;  
Pred. No. 41;  
RESULT 779  
ID AAG42380 standard; protein; 1191 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52848.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match Best Local Similarity 6.4%; Score 77; DB 3; Length 1191;  
Pred. No. 49;  
RESULT 780  
ID AAG42379 standard; protein; 1202 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52847.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match Best Local Similarity 6.4%; Score 77; DB 3; Length 1202;  
Pred. No. 50;  
RESULT 781  
ID AAR29527 standard; protein; 2510 AA.  
DE HCV antigen T7N1-30.  
PN EPI18313-A2.  
PD 16-DEC-1992.  
PA (MITU) MITSUBISHI KASEI CORP.  
Query Match Best Local Similarity 6.4%; Score 77; DB 2; Length 2510;  
Pred. No. 1.4e+02;  
RESULT 782  
ID ADX40818 standard; protein; 3010 AA.  
DE HCV polymerase protein #41.  
PN WO2005012502-A2.  
PD 10-FEB-2005.  
PA (EPIM-) EPIMUNE INC.  
Query Match Best Local Similarity 6.4%; Score 77; DB 9; Length 3010;  
Pred. No. 1.8e+02;  
RESULT 783  
ID ADX40816 standard; protein; 3010 AA.  
DE HCV polymerase protein #39.  
PN WO2005012502-A2.  
PD 10-FEB-2005.  
PA (EPIM-) EPIMUNE INC.  
Query Match Best Local Similarity 6.4%; Score 77; DB 9; Length 3010;  
Pred. No. 1.8e+02;  
RESULT 784  
ID ADR56855 standard; protein; 195 AA.  
DE Plant polypeptide, SEQ ID 6932.  
PN US2004216190-A1.  
PD 28-OCT-2004.  
PA (KOVA/) KOVALIC D K.  
Query Match Best Local Similarity 6.4%; Score 76.5; DB 8; Length 195;  
Pred. No. 4.6;  
RESULT 785  
ID ADR74966 standard; protein; 249 AA.  
DE Human 164-1h protein (seqid 25).  
PN WO2003097686-A1.  
PD 27-NOV-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match Best Local Similarity 6.4%; Score 76.5; DB 8; Length 249;  
Pred. No. 6.4;  
RESULT 786  
ID ADC01137 standard; protein; 278 AA.  
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 1181.  
PN JP2002355074-A.  
PD 10-DEC-2002.  
PA (UYTS-) UNIV TSUKUBA.  
Query Match Best Local Similarity 6.4%; Score 76.5; DB 7; Length 278;  
Pred. No. 7.5;  
RESULT 787  
ID ABO65827 standard; protein; 435 AA.  
DE Klebsiella pneumoniae polypeptide seqid 12344.  
PN US6610836-B1.

PD	26-AUG-2003.
PA	(GENO-) GENOME THERAPEUTICS CORP.
ID	AAD7984 standard; protein, 481 AA.
DE	Human 164-1b protein (SegID 28).
PB	WO2003097666-A1.
PN	MO2003097666-A1.
PD	27-NOV-2003.
PA	(TAKE ) TAKEDA CHEM IND LTD.
ID	AAR90765 standard; protein, 494 AA.
DE	Human K+ channel 2 mature protein.
PN	WO9603415-A1.
PD	08-FEB-1996.
PA	(HUMA-) HUMAN GENOME SCI INC.
ID	AAW42996 standard; protein, 494 AA.
DE	Purative mature potassium channel 2 protein.
PN	US5710019-A.
PD	20-JAN-1998.
PA	(HOMA-) HUMAN GENOME SCT INC.
ID	ABP58356 standard; protein, 494 AA.
DE	Human potassium channel subunit Kv5.1.
PN	WO200296944-A2.
PD	05-DEC-2002.
PA	(VLAA-) VLAAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
ID	ADC91A55 standard; protein, 494 AA.
DE	Human mature K+ channel 2 protein.
PN	US2003092895-A1.
PD	15-MAY-2003.
PA	(LIYY/) LI Y.
PA	(LITTY/) ADAMS M D.
PA	(WHIT/) WHITE O R.
ID	AAM20085 standard; protein, 509 AA.
DE	Helicobacter pylori cytoplasmic protein, 10009666 aa.
PN	WO9640893-A1.
PD	19-DEC-1996.
PA	(ASTR) ASTRA AB.
ID	ADO07984 standard; protein, 526 AA.
DE	Human hypothetical protein FLT203711-encoding cDNA.
PN	WO2004061123-A2.
PD	22-JUL-2004.
PA	(EXEL-) EXELIXIS INC.
ID	ADB25065 standard; protein, 526 AA.
DE	PRO polypeptide SEQ ID NO:2243.
PN	WO2004041170-A2.
PD	21-MAY-2004.
PA	(GEHT ) GENENTECH INC.
ID	AAU06638 standard; protein, 526 AA.
DE	Noel bronchial cancer-associated human protein SegID864.

[illegible]



Query Match 6.4%; Score 76; DB 3; Length 287;  
Best Local Similarity 26.7%; Pred. No. 8.9;  
RESULT 805  
ID AD096244 standard; protein; 366 AA.  
DE T cell activation associated protein #211.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH1 KASEI PHARMA CORP.  
Query Match 6.4%; Score 76; DB 8; Length 366;  
Best Local Similarity 22.0%; Pred. No. 13;  
RESULT 806  
ID AD096246 standard; protein; 366 AA.  
DE T cell activation associated protein #212.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH1 KASEI PHARMA CORP.  
Query Match 6.4%; Score 76; DB 8; Length 366;  
Best Local Similarity 22.0%; Pred. No. 13;  
RESULT 807  
ID ABB89424 standard; protein; 456 AA.  
DE Human polypeptide SEQ ID NO 1800.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.4%; Score 76; DB 5; Length 456;  
Best Local Similarity 22.0%; Pred. No. 17;  
RESULT 808  
ID AAB53400 standard; protein; 557 AA.  
DE Human colon cancer antigen protein sequence SEQ ID NO:940.  
PN WO200055351-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.4%; Score 76; DB 3; Length 557;  
Best Local Similarity 22.0%; Pred. No. 22;  
RESULT 809  
ID AAY44945 standard; protein; 593 AA.  
DE Wheat sulphate permease-2.  
PN WO200004154-A2.  
PD 27-JAN-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 6.4%; Score 76; DB 3; Length 593;  
Best Local Similarity 21.4%; Pred. No. 24;  
RESULT 810  
ID ADN22849 standard; protein; 1402 AA.  
DE Bacterial polypeptide #5502.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.4%; Score 76; DB 8; Length 1402;  
Best Local Similarity 20.2%; Pred. No. 81;  
RESULT 811  
ID ADN23383 standard; protein; 1917 AA.  
DE Bacterial polypeptide #6036.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.4%; Score 76; DB 8; Length 1917;  
Best Local Similarity 18.5%; Pred. No. 1.2e+02;  
RESULT 812  
ID ADX40794 standard; protein; 3010 AA.  
DE HCV polymerase protein #17.  
PN WO2005012502-A2.  
PD 10-FEB-2005.  
PA (EPIM-) EPIMUNE INC.  
Query Match 6.4%; Score 76; DB 9; Length 3010;

Best Local Similarity 25.4%; Pred. No. 2.3e+02;  
RESULT 813  
ID ADX40791 standard; protein; 3010 AA.  
DE HCV polymerase protein #14.  
PN WO2005012502-A2.  
PD 10-FEB-2005.  
PA (EPIM-) EPIMUNE INC.  
Query Match 6.4%; Score 76; DB 9; Length 3010;  
Best Local Similarity 25.4%; Pred. No. 2.3e+02;  
RESULT 814  
ID ADX40792 standard; protein; 3010 AA.  
DE HCV polymerase protein #15.  
PN WO2005012502-A2.  
PD 10-FEB-2005.  
PA (EPIM-) EPIMUNE INC.  
Query Match 6.4%; Score 76; DB 9; Length 3010;  
Best Local Similarity 26.9%; Pred. No. 2.3e+02;  
RESULT 815  
ID ABB63150 standard; protein; 228 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 16242.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.3%; Score 75.5; DB 4; Length 228;  
Best Local Similarity 21.8%; Pred. No. 7.4;  
RESULT 816  
ID ADX46633 standard; protein; 263 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 3148.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.3%; Score 75.5; DB 8; Length 263;  
Best Local Similarity 18.0%; Pred. No. 9.1;  
RESULT 817  
ID ADM92206 standard; protein; 263 AA.  
DE S pneumoniae antigenic protein sequence SeqID403.  
PN WO2004020609-A2.  
PD 11-MAR-2004.  
PA (TUFT) UNIV TUFTS.  
Query Match 6.3%; Score 75.5; DB 8; Length 263;  
Best Local Similarity 18.0%; Pred. No. 9.1;  
RESULT 818  
ID AAY81619 standard; protein; 264 AA.  
DE Streptococcus pneumoniae type 4 protein sequence #119.  
PN WO200006737-A2.  
PD 10-FEB-2000.  
PA (MICR-) MICROBIAL TECHNIQS LTD.  
Query Match 6.3%; Score 75.5; DB 3; Length 264;  
Best Local Similarity 18.0%; Pred. No. 9.1;  
RESULT 819  
ID ADR96242 standard; protein; 264 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 4877.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.3%; Score 75.5; DB 8; Length 264;  
Best Local Similarity 18.0%; Pred. No. 9.1;  
RESULT 820  
ID ABA60112 standard; protein; 264 AA.  
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:4877.  
PN US2005136404-A1.  
PD 23-JUN-2005.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 6.3%; Score 75.5; DB 9; Length 264;  
Best Local Similarity 18.0%; Pred. No. 9.1;  
RESULT 821  
ID ABB02182 standard; protein; 276 AA.  
DE S. pneumoniae type 4 strain protein from coding region #1759.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.

Query Match 6.3%; Score 75.5; DB 6; Length 276;  
Best Local Similarity 18.0%; Pred. No. 9.7;  
RESULT 822  
ID ABG93285 standard; protein; 342 AA.  
DE C. albicans BAX-associated protein fragment SEQ ID 528.  
PN WO200264766-A2.  
PD 22-AUG-2002.  
PA (JANC) JANSSEN PHARM NV.  
Query Match 6.3%; Score 75.5; DB 5; Length 342;  
Best Local Similarity 21.9%; Pred. No. 13;  
RESULT 823  
ID AAB15936 standard; protein; 352 AA.  
DE E. coli proliferation associated protein sequence SEQ ID NO:293.  
PN WO200044906-A2.  
PD 03-AUG-2000.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.3%; Score 75.5; DB 3; Length 352;  
Best Local Similarity 31.7%; Pred. No. 14;  
RESULT 824  
ID ADH51470 standard; protein; 363 AA.  
DE Rat MT1 receptor amino acid sequence #SEQ ID 2.  
PN FR935847-A1.  
PD 15-AUG-2003.  
PA (SERV-) LES LAB SERVIR SA.  
Query Match 6.3%; Score 75.5; DB 7; Length 363;  
Best Local Similarity 23.5%; Pred. No. 14;  
RESULT 825  
ID AAU03851 standard; protein; 397 AA.  
DE G protein-coupled receptor-like (GPCR-like) receptor protein #23.  
PN WO200138533-A2.  
PD 31-MAY-2001.  
PA (PHAA) PHARMACIA & UPJOHN.  
Query Match 6.3%; Score 75.5; DB 4; Length 397;  
Best Local Similarity 19.1%; Pred. No. 16;  
RESULT 826  
ID ADU92092 standard; protein; 415 AA.  
DE Escherichia coli TnaB protein.  
PN EP1484410-A1.  
PD 08-DEC-2004.  
PA (AJTN) AJINOMOTO KK.  
Query Match 6.3%; Score 75.5; DB 9; Length 415;  
Best Local Similarity 20.5%; Pred. No. 17;  
RESULT 827  
ID AEB41698 standard; protein; 430 AA.  
DE L. pneumophila protein SEQ ID NO 6030.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP) INST PASTEUR.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 6.3%; Score 75.5; DB 9; Length 430;  
Best Local Similarity 25.3%; Pred. No. 18;  
RESULT 828  
ID AAU03852 standard; protein; 433 AA.  
DE G protein-coupled receptor-like (GPCR-like) receptor protein #24.  
PN WO200138533-A2.  
PD 31-MAY-2001.  
PA (PHAA) PHARMACIA & UPJOHN.  
Query Match 6.3%; Score 75.5; DB 4; Length 433;  
Best Local Similarity 19.1%; Pred. No. 18;  
RESULT 829  
ID AEB38437 standard; protein; 436 AA.  
DE L. pneumophila protein SEQ ID NO 2769.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP) INST PASTEUR.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 6.3%; Score 75.5; DB 9; Length 436;  
Best Local Similarity 25.5%; Pred. No. 18;  
RESULT 830

ID ADS24239 standard; protein; 463 AA.  
DE Bacterial polypeptide #13272.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.3%; Score 75.5; DB 8; Length 463;  
Best Local Similarity 21.4%; Pred. No. 20;  
RESULT 831  
ID ADO29507 standard; protein; 471 AA.  
DE Mouse GPCR HTR2A, SEQ ID NO:609.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 6.3%; Score 75.5; DB 8; Length 471;  
Best Local Similarity 21.0%; Pred. No. 20;  
RESULT 832  
ID AAU03820 standard; protein; 499 AA.  
DE G protein-coupled receptor-like (GPCR-like) receptor protein #19.  
PN WO200138533-A2.  
PD 31-MAY-2001.  
PA (PHAA) PHARMACIA & UPJOHN.  
Query Match 6.3%; Score 75.5; DB 4; Length 499;  
Best Local Similarity 19.1%; Pred. No. 22;  
RESULT 833  
ID ADM72132 standard; protein; 392 AA.  
DE Human NTRAN polypeptide (clone ID 7524555CD1).  
PN WO2004022705-A2.  
PD 18-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.3%; Score 75; DB 8; Length 392;  
Best Local Similarity 21.0%; Pred. No. 18;  
RESULT 834  
ID AEM90212 standard; protein; 404 AA.  
DE Rice abiotic stress responsive polypeptide SEQ ID NO:8934.  
PN WO2003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 6.3%; Score 75; DB 7; Length 404;  
Best Local Similarity 15.6%; Pred. No. 19;  
RESULT 835  
ID AEB39222 standard; protein; 418 AA.  
DE L. pneumophila protein SEQ ID NO 3554.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP) INST PASTEUR.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 6.3%; Score 75; DB 9; Length 418;  
Best Local Similarity 20.7%; Pred. No. 20;  
RESULT 836  
ID AEB35772 standard; protein; 437 AA.  
DE L. pneumophila protein SEQ ID NO 104.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP) INST PASTEUR.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 6.3%; Score 75; DB 9; Length 437;  
Best Local Similarity 20.7%; Pred. No. 21;  
RESULT 837  
ID AAU45917 standard; protein; 445 AA.  
DE Propionibacterium acnes immunogenic protein #6813.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (COR-) CORIXA CORP.  
Query Match 6.3%; Score 75; DB 4; Length 445;  
Best Local Similarity 24.8%; Pred. No. 22;

RESULT 838  
ID ASM42436 standard; protein; 445 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7112.  
PN W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 6.3%; Score 75; DB 6; Length 445;  
Best Local Similarity 24.8%; Pred. No. 22;  
RESULT 839  
ID AAM87563 standard; protein; 452 AA.  
DE Rice abiotic stress responsive polypeptide SEQ ID NO:5809.  
PN W02003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
Query Match 6.3%; Score 75; DB 7; Length 452;  
Best Local Similarity 15.6%; Pred. No. 22;  
RESULT 840  
ID ADA34178 standard; protein; 467 AA.  
DE Acinetobacter baumannii protein #1339.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.3%; Score 75; DB 6; Length 467;  
Best Local Similarity 23.1%; Pred. No. 23;  
RESULT 841  
ID ADR14597 standard; protein; 473 AA.  
DE Human NF-kappaB pathway-associated protein SeqID598.  
PN W0200406557-A2.  
PD 05-AUG-2004.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match 6.3%; Score 75; DB 8; Length 473;  
Best Local Similarity 21.0%; Pred. No. 23;  
RESULT 842  
ID ADP99138 standard; protein; 480 AA.  
DE Human transporter and ion channel (TRICH) protein - SEQ ID 3.  
PN W02004048599-A2.  
PD 10-JUN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 6.3%; Score 75; DB 8; Length 480;  
Best Local Similarity 21.0%; Pred. No. 24;  
RESULT 843  
ID ADH86490 standard; protein; 549 AA.  
DE Enterococcus faecalis polypeptide #970.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
Query Match 6.3%; Score 75; DB 7; Length 549;  
Best Local Similarity 18.7%; Pred. No. 29;  
RESULT 844  
ID ADX80121 standard; protein; 635 AA.  
DE Plant full length insert polypeptide seqid 49487.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LITU/) LITU J.  
PA (ZHOV/) ZHOV Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABV/) TABASKA J E.  
PA (CMOY/) CMO Y.  
Query Match 6.3%; Score 75; DB 8; Length 635;  
Best Local Similarity 25.3%; Pred. No. 35;  
RESULT 845  
ID AAR54066 standard; protein; 1051 AA.  
DE Non-A, non-B hepatitis virus gene #4 product.  
PN JP06141870-A.  
PD 24-MAY-1994.  
PA (TORR-) ZH TOKYOTO RINSO IGAKU SOGO KENKYUSHO.  
PA (SANT-) SAWA KAGAKU KENKYUSHO CO.  
PA (TOFU) TONEN CORP.  
Query Match 6.3%; Score 75; DB 2; Length 1051;  
Best Local Similarity 23.4%; Pred. No. 71;  
RESULT 846

ID AAR98361 standard; protein; 1051 AA.  
DE 5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).  
PN JP07133291-A.  
PD 23-MAY-1995.  
PA (TOFU) TONEN CORP.  
Query Match 6.3%; Score 75; DB 2; Length 1051;  
Best Local Similarity 23.4%; Pred. No. 71;  
RESULT 847  
ID ADB64712 standard; protein; 1131 AA.  
DE Human protein encoded by clone NT2NE20077270.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.3%; Score 75; DB 7; Length 1131;  
Best Local Similarity 23.9%; Pred. No. 79;  
RESULT 848  
ID ABB64494 standard; protein; 2248 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 20274.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (BEKE) PE CORP NY.  
Query Match 6.3%; Score 75; DB 4; Length 2248;  
Best Local Similarity 22.9%; Pred. No. 2e+02;  
RESULT 849  
ID ADG20763 standard; protein; 2248 AA.  
DE Drosophila melanogaster rutabaga protein SEQ ID NO:2.  
PN W02003103704-A2.  
PD 18-DEC-2003.  
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
Query Match 6.3%; Score 75; DB 8; Length 2248;  
Best Local Similarity 22.9%; Pred. No. 2e+02;  
RESULT 850  
ID ADQ89656 standard; protein; 2248 AA.  
DE Antagonist of cell cycle progression polypeptide #43.  
PN W02004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Query Match 6.3%; Score 75; DB 8; Length 2248;  
Best Local Similarity 22.9%; Pred. No. 2e+02;  
RESULT 851  
ID ADX40796 standard; protein; 3010 AA.  
DE HCV polymerase protein #19.  
PN W02005012502-A2.  
PD 10-FEB-2005.  
PA (EPIM-) EPIMUNE INC.  
Query Match 6.3%; Score 75; DB 9; Length 3010;  
Best Local Similarity 25.4%; Pred. No. 3.1e+02;  
RESULT 852  
ID AAB66797 standard; protein; 200 AA.  
DE Porcine reproductive and respiratory syndrome virus ORF #5 protein.  
PN W0200102858-A1.  
PD 11-JAN-2001.  
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.  
PA (MATE-) INST MATERIALS RES & ENG.  
Query Match 6.2%; Score 74.5; DB 4; Length 200;  
Best Local Similarity 23.8%; Pred. No. 8.1;  
RESULT 853  
ID ADF74954 standard; protein; 256 AA.  
DE Rat 164-1h protein (SeqID 13).  
PN W02003097686-A1.  
PD 27-NOV-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 6.2%; Score 74.5; DB 8; Length 256;  
Best Local Similarity 23.3%; Pred. No. 11;  
RESULT 854  
ID AAR53748 standard; protein; 355 AA.  
DE Seven transmembrane receptor (V28).  
PN W09412635-A2.  
PD 09-JUN-1994.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 2; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;

RESULT 855  
ID AAW48722 standard; protein; 355 AA.  
DE Human V28 seven transmembrane receptor.  
PN US5759804-A.  
PD 02-JUN-1998.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 2; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 856  
ID AAY90677 standard; protein; 355 AA.  
DE Human mutant G protein-coupled receptor V28 (I230K).  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 6.2%; Score 74.5; DB 3; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 857  
ID AAY90642 standard; protein; 355 AA.  
DE Human G protein-coupled receptor V28.  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 6.2%; Score 74.5; DB 3; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 858  
ID AAB21693 standard; protein; 355 AA.  
DE Human 7TM receptor V28 cDNA clone protein #2.  
PN US6107475-A.  
PD 22-AUG-2000.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 3; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 859  
ID AAB21692 standard; protein; 355 AA.  
DE Human 7TM receptor V28 cDNA clone protein #1.  
PN US6107475-A.  
PD 22-AUG-2000.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 3; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 860  
ID AAG80126 standard; protein; 355 AA.  
DE Human CX3CR1 protein.  
PN WO200172830-A2.  
PD 04-OCT-2001.  
PA (IPFP-) IPF PHARM GMBH.  
Query Match 6.2%; Score 74.5; DB 3; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 861  
ID AAB82786 standard; protein; 355 AA.  
DE Human CX3C chemokine receptor 1.  
PN WO200160406-A1.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.2%; Score 74.5; DB 4; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 862  
ID AAV91235 standard; protein; 355 AA.  
DE Human 7 transmembrane domain receptor V28 #2.  
PN US6348574-B1.  
PD 19-FEB-2002.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 5; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 863  
ID AAV91234 standard; protein; 355 AA.  
DE Human 7 transmembrane domain receptor V28 #1.  
PN US6348574-B1.  
PD 19-FEB-2002.  
PA (ICOS-) ICOS CORP.  
Query Match 6.2%; Score 74.5; DB 5; Length 355;

Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 864  
ID AAU94327 standard; protein; 355 AA.  
DE Protein CX3CR1 differentially expressed in breast cancer tissue.  
PN WO200210436-A2.  
PD 07-FEB-2002.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 6.2%; Score 74.5; DB 5; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 865  
ID ABR58524 standard; protein; 355 AA.  
DE Human chemokine (C-X3-C) receptor 1 protein.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOS-) EOS BIOTECHNOLOGY INC.  
Query Match 6.2%; Score 74.5; DB 6; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 866  
ID AAO29513 standard; protein; 355 AA.  
DE Human fractalkine receptor (313) protein.  
PN WO2003039475-A2.  
PD 15-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 6.2%; Score 74.5; DB 6; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 867  
ID AAP97732 standard; protein; 355 AA.  
DE Amino acid sequence of human chemokine receptor CX3CR1.  
PN WO2003014153-A2.  
PD 20-FEB-2003.  
PA (TOPI-) TOPIGEN PHARM INC.  
Query Match 6.2%; Score 74.5; DB 6; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 868  
ID AAP81882 standard; protein; 355 AA.  
DE Human CX3C chemokine fractalkine receptor 1 protein SEQ ID NO:249.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 6.2%; Score 74.5; DB 6; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 869  
ID ADC22751 standard; protein; 355 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #74.  
PN US6555339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 6.2%; Score 74.5; DB 7; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 870  
ID ADC22649 standard; protein; 355 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #34.  
PN US6555339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 6.2%; Score 74.5; DB 7; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 871  
ID ADH14224 standard; protein; 355 AA.  
DE Mutated human serotonin V28.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAM/) LIAM C W.  
Query Match 6.2%; Score 74.5; DB 7; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;  
RESULT 872  
ID ADH14122 standard; protein; 355 AA.  
DE Human serotonin V28.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (CHAL/) CHALMERS D T.  
Query Match 6.2%; Score 74.5; DB 7; Length 355;  
Best Local Similarity 25.8%; Pred. No. 18;

PA (LIAM/) LIAM C W.  
 PA (BEHA/) BEHAN D P.  
 PA (CHAL/) CHALMERS D T.  
 Query Match  
 Best Local Similarity 25.8%; Score 74.5; DB 7; Length 355;  
 RESULT 873  
 ID ADH10680 standard; protein; 355 AA.  
 DE Human CX3CR1 polypeptide.  
 PN WO2003104484-A1.  
 PD 18-DEC-2003.  
 PA (META-) METABOLEX INC.  
 Query Match  
 Best Local Similarity 25.8%; Score 74.5; DB 8; Length 355;  
 RESULT 874  
 ID ADO29269 standard; protein; 355 AA.  
 DE Human GPCR CX3CR1, SEQ ID NO:370.  
 PN WO2004040000-A2.  
 PD 13-MAY-2004.  
 PA (PRIM-) PRIMML INC.  
 Query Match  
 Best Local Similarity 25.8%; Score 74.5; DB 8; Length 355;  
 RESULT 875  
 ID ADO18141 standard; protein; 355 AA.  
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 958.  
 PN WO200404838-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match  
 Best Local Similarity 25.8%; Score 74.5; DB 8; Length 355;  
 RESULT 876  
 ID ADP56020 standard; protein; 355 AA.  
 DE Human PRO protein sequence SEQ ID NO:1996.  
 PN WO2004039956-A2.  
 PD 13-MAY-2004.  
 PA (GETH-) GENENTECH INC.  
 Query Match  
 Best Local Similarity 25.8%; Score 74.5; DB 8; Length 355;  
 RESULT 877  
 ID ADP54585 standard; protein; 355 AA.  
 DE Human PRO protein sequence SEQ ID NO:561.  
 PN WO2004039956-A2.  
 PD 13-MAY-2004.  
 PA (GETH-) GENENTECH INC.  
 Query Match  
 Best Local Similarity 25.8%; Score 74.5; DB 8; Length 355;  
 RESULT 878  
 ID ADP3931 standard; protein; 355 AA.  
 DE PRO polypeptide SEQ ID NO:1109.  
 PN WO2004041170-A2.  
 PD 21-MAY-2004.  
 PA (GETH-) GENENTECH INC.  
 Query Match  
 Best Local Similarity 25.8%; Score 74.5; DB 8; Length 355;  
 RESULT 879  
 ID ADQ39421 standard; protein; 355 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1084.  
 PN WO2004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match  
 Best Local Similarity 25.8%; Score 74.5; DB 8; Length 355;  
 RESULT 880  
 ID ADY15644 standard; protein; 355 AA.  
 DE PRO polypeptide SEQ ID NO 1450.  
 PN WO2005016962-A2.  
 PD 24-FEB-2005.  
 PA (GETH-) GENENTECH INC.  
 Query Match  
 Best Local Similarity 25.8%; Score 74.5; DB 9; Length 355;  
 RESULT 881  
 ID ADQ39422 standard; protein; 362 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1085.  
 PN WO2004058052-A2.

PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match  
 Best Local Similarity 25.8%; Score 74.5; DB 8; Length 362;  
 RESULT 882  
 ID AAW77109 standard; protein; 471 AA.  
 DE Rat 5-HT2A serotonin receptor C322K mutant.  
 PN WO9838217-A1.  
 PD 03-SEP-1998.  
 PA (TEIT/) TEITLER M.  
 PA (HERR/) HERRICK-DAVIS K.  
 PA (EGAN/) EGAN C C.  
 Query Match  
 Best Local Similarity 21.0%; Score 74.5; DB 2; Length 471;  
 RESULT 883  
 ID AAW77111 standard; protein; 471 AA.  
 DE Rat 5-HT2A serotonin receptor C322E mutant.  
 PN WO9838217-A1.  
 PD 03-SEP-1998.  
 PA (TEIT/) TEITLER M.  
 PA (HERR/) HERRICK-DAVIS K.  
 PA (EGAN/) EGAN C C.  
 Query Match  
 Best Local Similarity 21.0%; Score 74.5; DB 2; Length 471;  
 RESULT 884  
 ID AAW77110 standard; protein; 471 AA.  
 DE Rat 5-HT2A serotonin receptor C322R mutant.  
 PN WO9838217-A1.  
 PD 03-SEP-1998.  
 PA (TEIT/) TEITLER M.  
 PA (HERR/) HERRICK-DAVIS K.  
 PA (EGAN/) EGAN C C.  
 Query Match  
 Best Local Similarity 21.0%; Score 74.5; DB 2; Length 471;  
 RESULT 885  
 ID AAW77104 standard; protein; 471 AA.  
 DE Rat 5-HT2A serotonin receptor.  
 PN WO9838217-A1.  
 PD 03-SEP-1998.  
 PA (TEIT/) TEITLER M.  
 PA (HERR/) HERRICK-DAVIS K.  
 PA (EGAN/) EGAN C C.  
 Query Match  
 Best Local Similarity 21.0%; Score 74.5; DB 2; Length 471;  
 RESULT 886  
 ID ABB07980 standard; protein; 471 AA.  
 DE Rat 5-HT2 receptor sequence.  
 PN US6383762-B1.  
 PD 07-MAY-2002.  
 PA (SYNA-) SYNAPTIC PHARM CORP.  
 Query Match  
 Best Local Similarity 21.0%; Score 74.5; DB 5; Length 471;  
 RESULT 887  
 ID ADF74971 standard; protein; 481 AA.  
 DE Rat 164-1b protein (SegID 30).  
 PN WO2003097686-A1.  
 PD 27-NOV-2003.  
 PA (TAKE-) TAKEDA CHEM IND LTD.  
 Query Match  
 Best Local Similarity 23.3%; Score 74.5; DB 8; Length 481;  
 RESULT 888  
 ID AAM93692 standard; protein; 562 AA.  
 DE Human polypeptide, SEQ ID NO: 3602.  
 PN EP1130094-A2.  
 PD 05-SEP-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match  
 Best Local Similarity 23.1%; Score 74.5; DB 4; Length 562;  
 RESULT 889  
 ID ADJ31569 standard; protein; 562 AA.  
 DE Human protein encoded by a full length cDNA clone SegID 3602.  
 PN EP1396543-A2.  
 PD 10-MAR-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.2%; Score 74.5; DB 8; Length 562;  
Best Local Similarity 23.1%; Pred. No. 34;  
RESULT 890  
ID ADQ96138 standard; protein; 562 AA.  
DE T cell activation associated protein #158.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAMI KASEI PHARMA CORP.  
Query Match 6.2%; Score 74.5; DB 8; Length 562;  
Best Local Similarity 23.1%; Pred. No. 34;  
RESULT 891  
ID ADP66160 standard; protein; 587 AA.  
DE Aspergillus fumigatus essential gene protein #210.  
PN WO2004067709-A2.  
PD 12-AUG-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Query Match 6.2%; Score 74.5; DB 8; Length 587;  
Best Local Similarity 18.2%; Pred. No. 36;  
RESULT 892  
ID ABB62948 standard; protein; 597 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 15636.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.2%; Score 74.5; DB 4; Length 597;  
Best Local Similarity 27.2%; Pred. No. 37;  
RESULT 893  
ID ADX66440 standard; protein; 661 AA.  
DE Plant full length insert polypeptide seqid 37283.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUT/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABR/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match 6.2%; Score 74.5; DB 8; Length 661;  
Best Local Similarity 20.4%; Pred. No. 43;  
RESULT 894  
ID ADA36878 standard; protein; 940 AA.  
DE Acinetobacter baumannii protein #4039.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENC-) GENOME THERAPEUTICS CORP.  
Query Match 6.2%; Score 74.5; DB 6; Length 940;  
Best Local Similarity 21.1%; Pred. No. 70;  
RESULT 895  
ID ABB92731 standard; protein; 1808 AA.  
DE Herbicidially active polypeptide SEQ ID NO 1942.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB) BAYER AG.  
Query Match 6.2%; Score 74.5; DB 5; Length 1808;  
Best Local Similarity 17.3%; Pred. No. 1.7e+02;  
RESULT 896  
ID AAE20477 standard; protein; 3010 AA.  
DE HCV-S1 full-length polypeptide.  
PN WO200208447-A2.  
PD 31-JAN-2002.  
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
PA (EHRU/) EHRICH G.  
Query Match 6.2%; Score 74.5; DB 5; Length 3010;  
Best Local Similarity 23.8%; Pred. No. 3.5e+02;  
RESULT 897  
ID ADF07294 standard; protein; 154 AA.  
DE Bacterial polypeptide #3407.  
PN US665709-B1.  
PD 12-AUG-2003.  
PA (GENC-) GENOME THERAPEUTICS CORP.  
Query Match 6.2%; Score 74; DB 7; Length 154;  
Best Local Similarity 6.2%; Pred. No. 17;  
RESULT 898  
ID ABB54180 standard; protein; 312 AA.  
DE Lactococcus lactis protein y11G.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 6.2%; Score 74; DB 5; Length 312;  
Best Local Similarity 24.3%; Pred. No. 17;  
RESULT 901  
ID ADS44483 standard; protein; 312 AA.  
DE Bacterial polypeptide #22913.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 6.2%; Score 74; DB 8; Length 312;  
Best Local Similarity 38.3%; Pred. No. 17;  
RESULT 902  
ID ABU02869 standard; protein; 324 AA.  
DE S. pneumoniae type 4 strain protein from coding region #2450.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENC-) INST GENOMIC RES.  
Query Match 6.2%; Score 74; DB 6; Length 324;  
Best Local Similarity 24.3%; Pred. No. 18;  
RESULT 903  
ID ADR94027 standard; protein; 332 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 2662.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENC-) GENOME THERAPEUTICS CORP.  
Query Match 6.2%; Score 74; DB 8; Length 332;  
Best Local Similarity 24.3%; Pred. No. 19;  
RESULT 904  
ID AEA57897 standard; protein; 332 AA.  
DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:2662.  
PN US2005136404-A1.  
PD 23-JUN-2005.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 6.2%; Score 74; DB 9; Length 332;  
Best Local Similarity 24.3%; Pred. No. 19;  
RESULT 905  
ID ABO00448 standard; protein; 342 AA.  
DE Novel human polypeptide #35.  
PN WO2003023013-A2.  
PD 20-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.2%; Score 74; DB 6; Length 342;  
Best Local Similarity 21.2%; Pred. No. 20;  
RESULT 906  
ID AAR88412 standard; protein; 350 AA.

DE High-affinity melatonin-1a receptor.  
PN W09535320-A1.  
PD 28-DEC-1995.  
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 2; Length 350;  
RESULT 907  
ID AAM15786 standard; protein; 350 AA.  
DE Melatonin receptor protein.  
PN JF09084581-A.  
PD 31-MAR-1997.  
PA (TAKE ) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 2; Length 350;  
RESULT 908  
ID AAM94761 standard; protein; 350 AA.  
DE Human melatonin receptor protein mel-1a.  
PN EP892046-A2.  
PD 20-JAN-1999.  
PA (JCRP-) JCR PHARM CO LTD.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 2; Length 350;  
RESULT 909  
ID AAP81840 standard; protein; 350 AA.  
DE Human melatonin receptor type 1a protein SEQ ID NO:164.  
PN W0200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 6; Length 350;  
RESULT 910  
ID ADO29552 standard; protein; 350 AA.  
DE Human GPCR MTR1A, SEQ ID NO:654.  
PN W0200404000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 8; Length 350;  
RESULT 911  
ID AAM19320 standard; protein; 364 AA.  
DE Rat growth hormone secretagogue receptor type 1a.  
PN W09721730-A1.  
PD 19-JUN-1997.  
PA (MERI ) MERCK & CO INC.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 2; Length 364;  
RESULT 912  
ID ABM73179 standard; protein; 366 AA.  
DE Staphylococcus aureus protein #2419.  
PN W0200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 6; Length 366;  
RESULT 913  
ID ABB55224 standard; protein; 442 AA.  
DE Lactococcus lactis protein yted.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 5; Length 442;  
RESULT 914  
ID ADN23927 standard; protein; 485 AA.  
DE Bacterial polypeptide #6580.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOVY) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 8; Length 485;

Best Local Similarity 26.2%; Pred. No. 32;  
RESULT 915  
ID AAY80509 standard; protein; 492 AA.  
DE F. lutescens L-Lysine:2-oxoglutarate 6-aminotransferase.  
PN W0200008170-A1.  
PD 17-FEB-2000.  
PA (SAOC ) MERCIAN CORP.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 3; Length 492;  
RESULT 916  
ID AAG64105 standard; protein; 493 AA.  
DE Flavobacterium lutescens L-Lysine-6-aminotransferase.  
PN W0200148216-A1.  
PD 05-JUL-2001.  
PA (SAOC ) MERCIAN CORP.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 4; Length 493;  
RESULT 917  
ID AAR54067 standard; protein; 1031 AA.  
DE Non-A, non-B hepatitis virus gene #6 product.  
PN JF06141870-A.  
PD 24-MAY-1994.  
PA (TOKR-) ZH TOKYOOTO RINSHO IGAKU SOGO KENKYUSHO.  
PA (SANW ) SANWA KAGAKU KENKYUSHO CO.  
PA (TOFU ) TONEN CORP.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 2; Length 1031;  
RESULT 918  
ID AAR98362 standard; protein; 1031 AA.  
DE 5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#6).  
PN JF07133291-A.  
PD 23-MAY-1995.  
PA (TOFU ) TONEN CORP.  
Query Match  
Best Local Similarity 6.2%; Score 74; DB 2; Length 1031;  
RESULT 919  
ID AAG59839 standard; protein; 120 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77442.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 6.2%; Score 73.5; DB 3; Length 120;  
RESULT 920  
ID AAU25578 standard; protein; 192 AA.  
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #25.  
PN W0200162797-A2.  
PD 30-AUG-2001.  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
Query Match  
Best Local Similarity 6.2%; Score 73.5; DB 4; Length 192;  
RESULT 921  
ID ADU08915 standard; protein; 226 AA.  
DE Coronavirus membrane protein seqid 38.  
PN W02004096842-A2.  
PD 11-NOV-2004.  
PA (BCCA-) BC CANCER AGENCY.  
Query Match  
Best Local Similarity 6.2%; Score 73.5; DB 8; Length 226;  
RESULT 922  
ID ABQ44044 standard; protein; 268 AA.  
DE Protein encoded by Prokaryotic essential gene #29571.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 6.2%; Score 73.5; DB 6; Length 268;  
RESULT 923  
ID AAG32488 standard; protein; 282 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39200.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 6.2%; Score 73.5; DB 3; Length 282;

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RESULT 924
ID ADF05982 standard; protein; 312 AA.
DE Bacterial polypeptide #2095.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 17.4%; Pred. No. 20; Length 312;
RESULT 925
ID AAG51386 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65212.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match
Best Local Similarity 28.1%; Pred. No. 26; Length 377;
RESULT 926
ID AAG33487 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39199.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match
Best Local Similarity 28.1%; Pred. No. 26; Length 377;
RESULT 927
ID ABM92289 standard; protein; 400 AA.
DE M. xanthus protein sequence, seq id 11488.
PN US6833447-B1.
PD 21-DEC-2004.
PA (MONSANTO) MONSANTO TECHNOLOGY LLC.
Query Match
Best Local Similarity 23.3%; Pred. No. 28; Length 400;
RESULT 928
ID ADQ75734 standard; protein; 404 AA.
DE Codon optimised hCMV IE1 encoded exons 2 and 4.
PN WO2004058166-A2.
PD 15-JUL-2004.
PA (VICAL-) VICAL INC.
Query Match
Best Local Similarity 19.3%; Pred. No. 28; Length 404;
RESULT 929
ID AAG51385 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65211.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match
Best Local Similarity 28.1%; Pred. No. 32; Length 442;
RESULT 930
ID AAG32486 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39198.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match
Best Local Similarity 28.1%; Pred. No. 32; Length 442;
RESULT 931
ID AAG51384 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65210.
PN EP1033405-A2.
PD 06-SEP-2000.
PA
Query Match
Best Local Similarity 28.1%; Pred. No. 37; Length 489;
RESULT 932
ID AAB86544 standard; protein; 491 AA.
DE Human cytomegalovirus strain AD169 IE1 protein.
PN WO200163286-A2.
PD 30-AUG-2001.
PA (KERN/) KERN F.
Query Match
Best Local Similarity 19.3%; Pred. No. 37; Length 491;
RESULT 933
ID ADP12517 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #127.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 19.3%; Pred. No. 37; Length 491;
RESULT 934
ID ADP12518 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #128.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 19.3%; Pred. No. 37; Length 491;
RESULT 935
ID ADP12513 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #123.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 19.3%; Pred. No. 37; Length 491;
RESULT 936
ID ADP12514 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #124.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 19.3%; Pred. No. 37; Length 491;
RESULT 937
ID ADQ75725 standard; protein; 491 AA.
DE Wild type hCMV IE1.
PN WO2004058166-A2.
PD 15-JUL-2004.
PA (VICAL-) VICAL INC.
Query Match
Best Local Similarity 19.3%; Pred. No. 37; Length 491;
RESULT 938
ID ABP73574 standard; protein; 574 AA.
DE Candida albicans essential protein SEQ ID NO 7411.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 20.8%; Pred. No. 46; Length 574;
RESULT 939
ID ADS28278 standard; protein; 637 AA.
DE Bacterial polypeptide #17311.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 28.3%; Pred. No. 53; Length 637;
RESULT 940
ID ABG29128 standard; protein; 682 AA.
DE Novel human diagnostic protein #29119.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 20.0%; Pred. No. 58; Length 682;
RESULT 941
ID ABB61737 standard; protein; 1287 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12003.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 18.2%; Pred. No. 1.4e+02; Length 1287;
RESULT 942
ID ADS96670 standard; protein; 1287 AA.
DE Drosophila melanogaster protein, SEQ ID 291.
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PN W0200403999-A2.  
PD 13-MAY-2004.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 6.2%; Score 73.5; DB 8; Length 1287;  
Best Local Similarity 18.2%; Pred. No. 1.4e+02;  
RESULT 943  
ID AAR33214 standard; protein; 3033 AA.  
DE NANEH virus strain HC-J8 protein.  
PD EP532167-A2.  
PD 17-MAR-1993.  
PA (IMMO ) IMMUNO JAPAN INC.  
Query Match 6.2%; Score 73.5; DB 2; Length 3033;  
Best Local Similarity 27.4%; Pred. No. 4.6e+02;  
RESULT 944  
ID ABY03151 standard; protein; 7176 AA.  
DE Murine hepatitis virus polIab protein, SEQ:9897.  
PD W02004093360-A2.  
PD 28-OCT-2004.  
PA (CHIR ) CHIRON CORP.  
Query Match 6.2%; Score 73.5; DB 8; Length 7176;  
Best Local Similarity 26.4%; Pred. No. 1.5e+03;  
RESULT 945  
ID AAW20571 standard; protein; 114 AA.  
DE H pylori secreted or periplasmic protein 80257.aa.  
PD W09640893-A1.  
PD 19-DEC-1996.  
PA (ASTR ) ASTRA AB.  
Query Match 6.1%; Score 73; DB 2; Length 114;  
Best Local Similarity 21.6%; Pred. No. 5.6;  
RESULT 946  
ID AAU69567 standard; protein; 189 AA.  
DE Human G protein-coupled receptor from cDNA Seq-2643.  
PD W0200177330-A2.  
PD 18-OCT-2001.  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
Query Match 6.1%; Score 73; DB 5; Length 189;  
Best Local Similarity 20.3%; Pred. No. 11;  
RESULT 947  
ID ADC97146 standard; protein; 199 AA.  
DE E. faecium protein sequence SEQ ID 6773.  
PD US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.1%; Score 73; DB 7; Length 199;  
Best Local Similarity 22.6%; Pred. No. 12;  
RESULT 948  
ID ABP29367 standard; protein; 249 AA.  
DE Streptococcus polypeptide SEQ ID NO 7910.  
PD W0200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 6.1%; Score 73; DB 5; Length 249;  
Best Local Similarity 24.6%; Pred. No. 17;  
RESULT 949  
ID AAU87836 standard; protein; 272 AA.  
DE T. aureum 7091 elongase TEL01 from plasmid PRAT-4-A1.  
PD W0200208401-A2.  
PD 31-JAN-2002.  
PA (ABBO ) ABBOTT LAB.  
Query Match 6.1%; Score 73; DB 5; Length 272;  
Best Local Similarity 19.9%; Pred. No. 19;  
RESULT 950  
ID ADH80191 standard; protein; 272 AA.  
DE Fungal 7091 elongase protein seq id 75.  
PD US2003163845-A1.  
PD 28-AUG-2003.  
PA (MOKE/) MOKERJI P.  
PA (LEON/) LEON-YEONG LEONARD A.  
PA (HUAN/) HUANG Y.  
PA (PERE/) PEREIRA S L.  
Query Match 6.1%; Score 73; DB 8; Length 272;  
Best Local Similarity 19.9%; Pred. No. 19;

RESULT 951  
ID ADM12982 standard; protein; 272 AA.  
DE Elongase protein #55.  
PD US2005009140-A1.  
PD 13-JAN-2005.  
PA (MOKE/) MOKERJI P.  
PA (LEON/) LEONARD A B.  
PA (HUAN/) HUANG Y.  
PA (PERE/) PEREIRA S L.  
Query Match 6.1%; Score 73; DB 9; Length 272;  
Best Local Similarity 19.9%; Pred. No. 19;  
RESULT 952  
ID ABM73154 standard; protein; 290 AA.  
DE Staphylococcus aureus protein #2394.  
PD W0200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.1%; Score 73; DB 6; Length 290;  
Best Local Similarity 23.4%; Pred. No. 20;  
RESULT 953  
ID ABR47464 standard; protein; 322 AA.  
DE Breast cancer associated protein sequence SEQ ID NO:160.  
PD W02003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 6.1%; Score 73; DB 6; Length 322;  
Best Local Similarity 20.6%; Pred. No. 24;  
RESULT 954  
ID ADN61865 standard; protein; 349 AA.  
DE Human novel protein NOV42a.  
PD US2004043382-A1.  
PD 04-MAR-2004.  
PA (PAD1/) PADIGARU M.  
PA (SEPT/) SPYTEK K A.  
PA (SHEN/) SHENOY S G.  
PA (TAUP/) TAUPIER R J.  
PA (PENA/) PENA C B A.  
PA (LILL/) LI L.  
PA (ZERR/) ZERRHUSEN B D.  
PA (GUSE/) GUSEV V Y.  
PA (JIMW/) JI W.  
PA (GORM/) GORMAN L.  
PA (MILL/) MILLER C E.  
PA (KEKU/) KEKUDA R.  
PA (PATY/) PATTURAJAN M.  
PA (GANG/) GANGOLLI E A.  
PA (VERN/) VERNET C A M.  
PA (GUOX/) GUO X S.  
PA (TCHE/) TCHERNEV V T.  
PA (FERN/) FERNANDES F R.  
PA (CASM/) CASMAN S J.  
PA (MALY/) MALYANKAR U M.  
PA (GERL/) GERLACH V.  
PA (LITV/) LIU Y.  
PA (ANDR/) ANDERSON D W.  
PA (SPAD/) SPADERNA S K.  
PA (CATT/) CATTERTON E.  
PA (LEIT/) LEITE M W.  
PA (ZHON/) ZHONG H.  
PA (ALSO/) ALSOBROOK J P.  
PA (LEPL/) LEPLLEY D M.  
PA (RIEG/) RIEGER D K.  
PA (BURG/) BURGESS C E.  
Query Match 6.1%; Score 73; DB 8; Length 349;  
Best Local Similarity 24.0%; Pred. No. 26;  
RESULT 955  
ID AAM19613 standard; protein; 364 AA.  
DE Rat growth hormone secretagogue receptor type Ia.  
PD W09722004-A1.  
PD 19-JUN-1997.  
PA (MERI ) MERCK & CO INC.  
Query Match 6.1%; Score 73; DB 2; Length 364;  
Best Local Similarity 19.4%; Pred. No. 28;

RESULT 956  
ID AAY54565 standard; protein; 364 AA.  
DE A mouse growth hormone secretagogue receptor.  
PN WO200002918-A1.  
PD 20-JAN-2000.  
PA (MERI ) MERCK & CO INC.  
Query Match 6.1%; Score 73; DB 3; Length 364;  
Best Local Similarity 19.4%; Pred. No. 28;  
RESULT 957  
ID AAB97377 standard; protein; 364 AA.  
DE Rat growth hormone secretagogue receptor (GHSR) related protein.  
PN WO200133705-A1.  
PD 10-MAY-2001.  
PA (TAKEDA ) TAKEDA CHEM IND LTD.  
Query Match 6.1%; Score 73; DB 4; Length 364;  
Best Local Similarity 19.4%; Pred. No. 28;  
RESULT 958  
ID ADO29026 standard; protein; 364 AA.  
DE Mouse novel GPCR GHSR, SEQ ID NO:125.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 6.1%; Score 73; DB 8; Length 364;  
Best Local Similarity 19.4%; Pred. No. 28;  
RESULT 959  
ID AAM77773 standard; protein; 377 AA.  
DE Staphylococcus aureus protein of unknown function.  
PN EP841394-A2.  
PD 13-MAY-1998.  
PA (SMIX ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
Query Match 6.1%; Score 73; DB 2; Length 377;  
Best Local Similarity 23.3%; Pred. No. 29;  
RESULT 960  
ID AAG50065 standard; protein; 415 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63404.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 73; DB 3; Length 415;  
Best Local Similarity 19.8%; Pred. No. 34;  
RESULT 961  
ID AAG24013 standard; protein; 427 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27528.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 73; DB 3; Length 427;  
Best Local Similarity 22.0%; Pred. No. 35;  
RESULT 962  
ID AAG24012 standard; protein; 430 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27527.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 73; DB 3; Length 430;  
Best Local Similarity 22.0%; Pred. No. 35;  
RESULT 963  
ID ABU31419 standard; protein; 453 AA.  
DE Protein encoded by Prokaryotic essential gene #16946.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIR-) ELITRA PHARM INC.  
Query Match 6.1%; Score 73; DB 6; Length 453;  
Best Local Similarity 26.5%; Pred. No. 38;  
RESULT 964  
ID AEA16981 standard; protein; 469 AA.  
DE Arabidopsis thaliana protein #40.  
PN US2005125159-A1.  
PD 09-JUN-2005.  
PA (STBI/) STEIN J C.  
PA (CAOV/) CAO Y.  
Query Match 6.1%; Score 73; DB 9; Length 469;  
Best Local Similarity 19.8%; Pred. No. 40;  
RESULT 965  
ID AAG50064 standard; protein; 472 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 63403.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 73; DB 3; Length 472;  
Best Local Similarity 19.8%; Pred. No. 40;  
RESULT 966  
ID AAG50063 standard; protein; 474 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63402.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 73; DB 3; Length 474;  
Best Local Similarity 19.8%; Pred. No. 40;  
RESULT 967  
ID ABM70313 standard; protein; 490 AA.  
DE Photorhabdus luminescens protein sequence #3410.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 6.1%; Score 73; DB 6; Length 490;  
Best Local Similarity 24.6%; Pred. No. 42;  
RESULT 968  
ID AAY33766 standard; protein; 495 AA.  
DE hrv5.1 human brain-specific potassium channel.  
PN WO9941372-A1.  
PD 19-AUG-1999.  
PA (ZENE ) ZENECA LTD.  
Query Match 6.1%; Score 73; DB 2; Length 495;  
Best Local Similarity 23.2%; Pred. No. 43;  
RESULT 969  
ID ABO63300 standard; protein; 501 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9817.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 6.1%; Score 73; DB 7; Length 501;  
Best Local Similarity 26.5%; Pred. No. 44;  
RESULT 970  
ID ABP53583 standard; protein; 526 AA.  
DE Human NOV13b protein SEQ ID NO:30.  
PN WO200262899-A2.  
PD 15-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.1%; Score 73; DB 5; Length 526;  
Best Local Similarity 23.3%; Pred. No. 47;  
RESULT 971  
ID ADH42229 standard; protein; 526 AA.  
DE Novel human protein NOV50d.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.1%; Score 73; DB 8; Length 526;  
Best Local Similarity 23.3%; Pred. No. 47;  
RESULT 972  
ID ABU31136 standard; protein; 553 AA.  
DE Protein encoded by Prokaryotic essential gene #16663.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIR-) ELITRA PHARM INC.  
Query Match 6.1%; Score 73; DB 6; Length 553;  
Best Local Similarity 19.6%; Pred. No. 50;  
RESULT 973  
ID AAG24011 standard; protein; 556 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27526.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 73; DB 3; Length 556;  
Best Local Similarity 22.0%; Pred. No. 50;  
RESULT 974  
ID ADO96000 standard; protein; 608 AA.  
DE T cell activation associated protein #89.  
PN WO2004058805-A2.  
PD 15-JUL-2004.

PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 6.1%; Score 73; DB 8; Length 608;  
Best Local Similarity 19.5%; Pred. No. 57;  
RESULT 975  
ID ADR99134 standard; protein: 635 AA.  
DE Staphylococcus aureus protein #2357.  
PN WO2004078035-A2.  
PD 16-SEP-2004.  
PA (PARB-) BAYER PHARM CORP.  
Query Match 6.1%; Score 73; DB 8; Length 635;  
Best Local Similarity 19.5%; Pred. No. 61;  
RESULT 976  
ID ABR71311 standard; protein: 717 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40725.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 6.1%; Score 73; DB 4; Length 717;  
Best Local Similarity 21.3%; Pred. No. 72;  
RESULT 977  
ID AAW26673 standard; protein: 746 AA.  
DE Staphylococcus aureus spoIIIE protein.  
PN WO9726338-A1.  
PD 24-JUL-1997.  
PA (SMIK-) SMITHKLINE BEECHAM PLC.  
Query Match 6.1%; Score 73; DB 2; Length 746;  
Best Local Similarity 23.3%; Pred. No. 76;  
RESULT 978  
ID AAU37199 standard; protein: 748 AA.  
DE Staphylococcus aureus cellular proliferation protein #1369.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 73; DB 4; Length 748;  
Best Local Similarity 23.3%; Pred. No. 76;  
RESULT 979  
ID AAW88407 standard; protein: 750 AA.  
DE Human adult neural tissue secreted protein s195\_10.  
PN WO9857976-A1.  
PD 23-DEC-1998.  
PA (GENV-) GENETICS INST INC.  
Query Match 6.1%; Score 73; DB 2; Length 750;  
Best Local Similarity 19.5%; Pred. No. 76;  
RESULT 980  
ID AAW26672 standard; protein: 788 AA.  
DE Staphylococcus aureus spoIIIE protein.  
PN WO9726338-A1.  
PD 24-JUL-1997.  
PA (SMIK-) SMITHKLINE BEECHAM PLC.  
Query Match 6.1%; Score 73; DB 2; Length 788;  
Best Local Similarity 23.3%; Pred. No. 82;  
RESULT 981  
ID ABB42392 standard; protein: 788 AA.  
DE Protein encoded by Prokaryotic essential gene #27919.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 73; DB 6; Length 788;  
Best Local Similarity 23.3%; Pred. No. 82;  
RESULT 982  
ID AAU36734 standard; protein: 792 AA.  
DE Staphylococcus aureus cellular proliferation protein #904.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 73; DB 4; Length 792;  
Best Local Similarity 23.3%; Pred. No. 82;  
RESULT 983  
ID ABB19057 standard; protein: 792 AA.  
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 334.  
PN WO200259148-A2.  
PD 01-AUG-2002.  
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.

Query Match 6.1%; Score 73; DB 6; Length 792;  
Best Local Similarity 23.3%; Pred. No. 82;  
RESULT 984  
ID ABB71317 standard; protein: 792 AA.  
DE Staphylococcus aureus protein #2357.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.1%; Score 73; DB 6; Length 792;  
Best Local Similarity 23.3%; Pred. No. 82;  
RESULT 985  
ID AAW68466 standard; protein: 845 AA.  
DE Protein encoded by fragment #6 isolated from Hepatitis C virus genome.  
PN WO9825960-A1.  
PD 18-JUN-1998.  
PA (INGG-) CENT ING GENETICA & BIOTECHNOLOGIA.  
Query Match 6.1%; Score 73; DB 2; Length 845;  
Best Local Similarity 26.2%; Pred. No. 90;  
RESULT 986  
ID ADO95946 standard; protein: 910 AA.  
DE T cell activation associated protein #62.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 6.1%; Score 73; DB 8; Length 910;  
Best Local Similarity 19.5%; Pred. No. 1e+02;  
RESULT 987  
ID ABG24246 standard; protein: 913 AA.  
DE Novel human diagnostic protein #24237.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.1%; Score 73; DB 4; Length 913;  
Best Local Similarity 19.5%; Pred. No. 1e+02;  
RESULT 988  
ID AAM51861 standard; protein: 966 AA.  
DE Murine polycystic kidney disease protein 2.  
PN WO200177331-A1.  
PD 18-OCT-2001.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 6.1%; Score 73; DB 5; Length 966;  
Best Local Similarity 21.3%; Pred. No. 1.1e+02;  
RESULT 989  
ID ABB07819 standard; protein: 966 AA.  
DE Mouse polycystic kidney disease protein 2.  
PN US2002035056-A1.  
PD 21-MAR-2002.  
PA (CURT/) CURTIS R A J.  
PA (STLO/) STLOS-SANTIAGO I.  
Query Match 6.1%; Score 73; DB 5; Length 966;  
Best Local Similarity 21.3%; Pred. No. 1.1e+02;  
RESULT 990  
ID ADJ76159 standard; protein: 966 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1411.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 6.1%; Score 73; DB 8; Length 966;  
Best Local Similarity 21.3%; Pred. No. 1.1e+02;  
RESULT 991  
ID ADY66235 standard; protein: 966 AA.  
DE Polycystic kidney disease protein 2, SRQ ID 11.  
PN US2004248160-A1.  
PD 09-DEC-2004.  
PA (MILL-) MILLENIUM PHARM INC.  
Query Match 6.1%; Score 73; DB 9; Length 966;  
Best Local Similarity 21.3%; Pred. No. 1.1e+02;  
RESULT 992  
ID ADZ26335 standard; protein: 966 AA.  
DE Human hypoxia-responsive protein CNGH0002.1.  
PN WO2005033293-A2.  
PD 14-APR-2005.  
PA (CENZ-) CENTOCOR INC.

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Query Match
Best Local Similarity 6.1%; Score 73; DB 9; Length 966;
RESULT 993
ID ABG05866 standard; protein; 971 AA.
DE Novel human diagnostic protein #5857.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 4; Length 971;
RESULT 994
ID ADR99135 standard; protein; 971 AA.
DE Human protein similar to Yeast SSM4, TEB4, SEQ ID 141.
PN W02004078035-A2.
PD 16-SEP-2004.
PA (FARB-) BAYER PHARM CORP.
Query Match
Best Local Similarity 6.1%; Score 73; DB 8; Length 971;
RESULT 995
ID AD211480 standard; protein; 971 AA.
DE MARCH VI protein, SEQ ID 49.
PN US2005079613-A1.
PD 14-APR-2005.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match
Best Local Similarity 6.1%; Score 73; DB 9; Length 971;
RESULT 996
ID AD211490 standard; protein; 971 AA.
DE MARCH VI protein, SEQ ID 59.
PN US2005079613-A1.
PD 14-APR-2005.
PA (UYOR-) UNIV OREGON HEALTH SCI.
Query Match
Best Local Similarity 6.1%; Score 73; DB 9; Length 971;
RESULT 997
ID ABG07373 standard; protein; 976 AA.
DE Novel human diagnostic protein #7364.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 4; Length 976;
RESULT 998
ID ADX40795 standard; protein; 3010 AA.
DE HCV polymerase protein #18.
PN W02005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMUNE INC.
Query Match
Best Local Similarity 6.1%; Score 73; DB 9; Length 3010;
RESULT 999
ID ABU05456 standard; protein; 209 AA.
DE M. tuberculosis and M. leprae marker protein #107.
PN W0200274903-A2.
PD 26-SEP-2002.
PA (INSP-) INST PASTEUR.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 5; Length 209;
RESULT 1000
ID ABUL302 standard; protein; 222 AA.
DE Protein encoded by Prokaryotic essential gene #829.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) BLITRA PHARM INC.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 6; Length 222;
RESULT 1001
ID ADY24595 standard; protein; 274 AA.
DE Plant full length insert polypeptide seqid 72379.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 274;
RESULT 1002
ID ADX95386 standard; protein; 274 AA.
DE Plant full length insert polypeptide seqid 58050.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 274;
RESULT 1003
ID ABB53879 standard; protein; 307 AA.
DE Lactococcus lactis protein yfeg.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 5; Length 307;
RESULT 1004
ID ADY1066 standard; protein; 307 AA.
DE Plant full length insert polypeptide seqid 66483.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 307;
RESULT 1005
ID ADY11265 standard; protein; 307 AA.
DE Plant full length insert polypeptide seqid 67080.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 307;
RESULT 1006
ID ADY10993 standard; protein; 307 AA.
DE Plant full length insert polypeptide seqid 66808.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABAS/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.1%; Score 72.5; DB 8; Length 307;
RESULT 1007
ID ADY11014 standard; protein; 308 AA.
DE Plant full length insert polypeptide seqid 66829.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
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PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match  
Best Local Similarity 25.3%; Score 72.5; DB 8; Length 308;  
Pred. No. 25;  
RESULT 1008  
ID ADY10930 standard; protein; 310 AA.  
DE Plant full length insert polypeptide seqid 66745.  
PN US200403488-A1.  
PD 19-FEB-2004.  
PA (LTUJ/) LTU J.  
PA (ZHOV/) ZHOV Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match  
Best Local Similarity 25.3%; Score 72.5; DB 8; Length 310;  
Pred. No. 26;  
RESULT 1009  
ID ADY11546 standard; protein; 310 AA.  
DE Plant full length insert polypeptide seqid 67361.  
PN US200403488-A1.  
PD 19-FEB-2004.  
PA (LTUJ/) LTU J.  
PA (ZHOV/) ZHOV Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match  
Best Local Similarity 25.3%; Score 72.5; DB 8; Length 310;  
Pred. No. 26;  
RESULT 1010  
ID ADY09462 standard; protein; 311 AA.  
DE Plant full length insert polypeptide seqid 65277.  
PN US200403488-A1.  
PD 19-FEB-2004.  
PA (LTUJ/) LTU J.  
PA (ZHOV/) ZHOV Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match  
Best Local Similarity 25.3%; Score 72.5; DB 8; Length 311;  
Pred. No. 26;  
RESULT 1011  
ID ADY11115 standard; protein; 312 AA.  
DE Plant full length insert polypeptide seqid 66930.  
PN US200403488-A1.  
PD 19-FEB-2004.  
PA (LTUJ/) LTU J.  
PA (ZHOV/) ZHOV Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match  
Best Local Similarity 25.3%; Score 72.5; DB 8; Length 312;  
Pred. No. 26;  
RESULT 1012  
ID ADY10946 standard; protein; 312 AA.  
DE Plant full length insert polypeptide seqid 66761.  
PN US200403488-A1.  
PD 19-FEB-2004.  
PA (LTUJ/) LTU J.  
PA (ZHOV/) ZHOV Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOV/) CAO Y.  
Query Match  
Best Local Similarity 25.3%; Score 72.5; DB 8; Length 312;  
Pred. No. 26;  
RESULT 1013  
ID AB853675 standard; protein; 325 AA.

DE Lactococcus lactis protein ydhb.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match  
Best Local Similarity 25.9%; Score 72.5; DB 5; Length 325;  
Pred. No. 27;  
RESULT 1014  
ID ADH87677 standard; protein; 353 AA.  
DE Enterococcus faecalis polypeptide #2157.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match  
Best Local Similarity 21.5%; Score 72.5; DB 7; Length 353;  
Pred. No. 31;  
RESULT 1015  
ID ADH87557 standard; protein; 359 AA.  
DE Enterococcus faecalis polypeptide #2037.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match  
Best Local Similarity 25.0%; Score 72.5; DB 7; Length 359;  
Pred. No. 31;  
RESULT 1016  
ID AAR37264 standard; protein; 389 AA.  
DE Oxytocin receptor.  
PN EP542424-A1.  
PD 19-MAY-1993.  
PA (ROHT ) ROHTO PHARM CO LTD.  
Query Match  
Best Local Similarity 24.5%; Score 72.5; DB 2; Length 389;  
Pred. No. 35;  
RESULT 1017  
ID AAW23832 standard; protein; 389 AA.  
DE Human oxytocin receptor.  
PN EP811684-A2.  
PD 10-DEC-1997.  
PA (ROHT ) ROHTO PHARM CO LTD.  
Query Match  
Best Local Similarity 24.5%; Score 72.5; DB 2; Length 389;  
Pred. No. 35;  
RESULT 1018  
ID AAM40217 standard; protein; 389 AA.  
DE Human polypeptide SEQ ID NO 3362.  
PN WO200153312-A1.  
PD 26-JUN-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 24.5%; Score 72.5; DB 4; Length 389;  
Pred. No. 35;  
RESULT 1019  
ID ABP81865 standard; protein; 389 AA.  
DE Human oxytocin receptor protein SEQ ID NO:215.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match  
Best Local Similarity 24.5%; Score 72.5; DB 6; Length 389;  
Pred. No. 35;  
RESULT 1020  
ID AAE38317 standard; protein; 389 AA.  
DE Human oxytocin receptor protein.  
PN WO2003064402-A1.  
PD 07-AUG-2003.  
PA (PRIZ ) PRIZER LTD.  
PA (PRIZ ) PRIZER INC.  
Query Match  
Best Local Similarity 24.5%; Score 72.5; DB 6; Length 389;  
Pred. No. 35;  
RESULT 1021  
ID ADF12125 standard; protein; 389 AA.  
DE Human oxytocin receptor (OXTR) protein SEQ ID NO:2.  
PN WO2003093816-A2.  
PD 13-NOV-2003.  
PA (FARB ) BAYER AG.  
Query Match  
Best Local Similarity 24.5%; Score 72.5; DB 8; Length 389;  
Pred. No. 35;

RESULT 1022  
ID ADI03915 standard; protein; 389 AA.  
DE Human oxytocin receptor polypeptide.  
PN W0200400093-A2.  
PD 31-DEC-2003.  
PA (UYOU-) UNIV QUEBEC A MONTREAL.  
(UYMO-) UNIV MONTREAL CENT HOSPITALIER.  
Query Match  
Best Local Similarity 24.5%; Score 72.5; DB 8; Length 389;  
Pred. No. 35;  
RESULT 1023  
ID ADO29590 standard; protein; 389 AA.  
DE Human GPCR OXTR, SEQ ID NO:692.  
PN W02004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match  
Best Local Similarity 24.5%; Score 72.5; DB 8; Length 389;  
Pred. No. 35;  
RESULT 1024  
ID ADM98687 standard; protein; 389 AA.  
DE Human oxytocin receptor (OXTR) protein SeqID1.  
PN W02005012565-A1.  
PD 10-FEB-2005.  
PA (ASTR-) ASTRAZENECA AB.  
(ASTR-) ASTRAZENECA UK LTD.  
Query Match  
Best Local Similarity 24.5%; Score 72.5; DB 9; Length 389;  
Pred. No. 35;  
RESULT 1025  
ID AAR58665 standard; protein; 448 AA.  
DE Bovine PACAP receptor type 1B mature protein.  
PN EP618291-A2.  
PD 05-OCT-1994.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 29.6%; Score 72.5; DB 2; Length 448;  
Pred. No. 43;  
RESULT 1026  
ID AAR58663 standard; protein; 476 AA.  
DE Bovine PACAP receptor type 1A mature protein.  
PN EP618291-A2.  
PD 05-OCT-1994.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 29.6%; Score 72.5; DB 2; Length 476;  
Pred. No. 47;  
RESULT 1027  
ID AAR58657 standard; protein; 485 AA.  
DE Bovine PACAP receptor type 1B protein.  
PN EP618291-A2.  
PD 05-OCT-1994.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 29.6%; Score 72.5; DB 2; Length 485;  
Pred. No. 48;  
RESULT 1028  
ID AAR58655 standard; protein; 513 AA.  
DE Bovine PACAP receptor type 1A protein.  
PN EP618291-A2.  
PD 05-OCT-1994.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match  
Best Local Similarity 29.6%; Score 72.5; DB 2; Length 513;  
Pred. No. 52;  
RESULT 1029  
ID ADN19765 standard; protein; 522 AA.  
DE Bacterial polypeptide #2418.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY-) CAO Y.  
(HINK-) HINKLE G J.  
(SIAT-) SLATER S C.  
(CHEN-) CHEN X.  
(GOLD-) GOLDMAN B S.  
Query Match  
Best Local Similarity 22.5%; Score 72.5; DB 8; Length 522;  
Pred. No. 53;  
RESULT 1030  
ID ADV8915 standard; protein; 666 AA.  
DE Streptococcus agalactiae protein sequence, SEQ ID 1509.

PN FR2824074-A1.  
PD 31-OCT-2002.  
PA (INSP-) INST PASTEUR.  
(CNRS) CNRS CENT NAT RECH SCI.  
Query Match  
Best Local Similarity 23.1%; Score 72.5; DB 8; Length 666;  
Pred. No. 74;  
RESULT 1031  
ID ADV82479 standard; protein; 666 AA.  
DE Streptococcus agalactiae protein, SEQ ID 3620.  
PN W0200292818-A2.  
PD 21-NOV-2002.  
PA (INSP-) INST PASTEUR.  
(CNRS) CNRS CENT NAT RECH SCI.  
Query Match  
Best Local Similarity 23.1%; Score 72.5; DB 8; Length 666;  
Pred. No. 74;  
RESULT 1032  
ID ADV80368 standard; protein; 666 AA.  
DE Streptococcus agalactiae protein, SEQ ID 1509.  
PN W0200292818-A2.  
PD 21-NOV-2002.  
PA (INSP-) INST PASTEUR.  
(CNRS) CNRS CENT NAT RECH SCI.  
Query Match  
Best Local Similarity 23.1%; Score 72.5; DB 8; Length 666;  
Pred. No. 74;  
RESULT 1033  
ID ADI81620 standard; protein; 769 AA.  
DE C. elegans protein similar to Pfam PF00023.  
PN US2004008537-A1.  
PD 15-JAN-2004.  
PA (ROOS-) ROOS J.  
(STAU-) STAUDERMAN K.  
(VELI-) VELICELEBI G.  
Query Match  
Best Local Similarity 20.2%; Score 72.5; DB 8; Length 769;  
Pred. No. 91;  
RESULT 1034  
ID ABB05429 standard; protein; 848 AA.  
DE Arabidopsis thaliana ABH1 protein SEQ ID NO:2.  
PN W0200196585-A2.  
PD 20-DEC-2001.  
PA (REGC-) UNIV CALIFORNIA.  
Query Match  
Best Local Similarity 22.3%; Score 72.5; DB 5; Length 848;  
Pred. No. 1e+02;  
RESULT 1035  
ID AAE31528 standard; protein; 848 AA.  
DE Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.  
PN W0200281696-A2.  
PD 17-OCT-2002.  
PA (SYGN-) SYNSENTA PARTICIPATIONS AG.  
Query Match  
Best Local Similarity 22.3%; Score 72.5; DB 6; Length 848;  
Pred. No. 1e+02;  
RESULT 1036  
ID ABU25159 standard; protein; 851 AA.  
DE Protein encoded by Prokaryotic essential gene #10686.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 20.5%; Score 72.5; DB 6; Length 851;  
Pred. No. 1e+02;  
RESULT 1037  
ID ADY10144 standard; protein; 903 AA.  
DE Plant full length insert polypeptide seqid 65959.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIUJ-) LIU J.  
(ZHOU-) ZHOU Y.  
(KOVA-) KOVALIC D K.  
(SCRE-) SCREEN S E.  
(TABAJ-) TABASKA J E.  
(CAOY-) CAO Y.  
Query Match  
Best Local Similarity 18.1%; Score 72.5; DB 8; Length 903;  
Pred. No. 1.1e+02;  
RESULT 1038  
ID ADW76078 standard; protein; 1051 AA.

DE Human cytomagalovirus (HCMV) pp65-IE1 fusion protein.  
PN WO2005007689-A1.  
PD 27-JAN-2005.  
PA (ALPH-) ALPHAVAX INC.  
Query Match 6.1%; Score 72.5; DB 9; Length 1051;  
Best Local Similarity 19.3%; Pred. No. 1.4e+02;  
RESULT 1039  
ID AAR34580 standard; protein; 3010 AA.  
DE Human hepatitis C virus gene encoded polypeptide.  
PN EP541089-A2.  
PD 12-MAY-1993.  
PA (SANY) SANWA KAGAKU KENKYUSHO CO.  
Query Match 6.1%; Score 72.5; DB 2; Length 3010;  
Best Local Similarity 23.7%; Pred. No. 6e+02;  
RESULT 1040  
ID ADO96378 standard; protein; 208 AA.  
DE T cell activation associated protein #278.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH I KASEI PHARMA CORP.  
Query Match 6.0%; Score 72; DB 8; Length 208;  
Best Local Similarity 20.8%; Pred. No. 17;  
RESULT 1041  
ID ABB46543 standard; protein; 306 AA.  
DE Listeria monocytogenes protein #1247.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP) INST PASTEUR.  
Query Match 6.0%; Score 72; DB 5; Length 306;  
Best Local Similarity 21.0%; Pred. No. 29;  
RESULT 1042  
ID ABU93432 standard; protein; 317 AA.  
DE Protein encoded by prokaryotic essential gene #24959.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 72; DB 6; Length 317;  
Best Local Similarity 23.5%; Pred. No. 30;  
RESULT 1043  
ID AAB53392 standard; protein; 334 AA.  
DE Human colon cancer antigen protein sequence SEQ ID NO:932.  
PN WO200055551-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 6.0%; Score 72; DB 3; Length 334;  
Best Local Similarity 28.8%; Pred. No. 33;  
RESULT 1044  
ID AAY87505 standard; protein; 370 AA.  
DE Human G coupled-protein receptor, hGR3.  
PN WO200017641-A1.  
PD 30-MAR-2000.  
PA (MILL-) MILENNIUM PHARM INC.  
Query Match 6.0%; Score 72; DB 3; Length 370;  
Best Local Similarity 21.8%; Pred. No. 38;  
RESULT 1045  
ID AAW20731 standard; protein; 375 AA.  
DE H. pylori inner membrane protein, O6cp1118orf6.  
PN WO9640893-A1.  
PD 19-DEC-1996.  
PA (ASTR-) ASTRA AB.  
Query Match 6.0%; Score 72; DB 2; Length 375;  
Best Local Similarity 20.9%; Pred. No. 38;  
RESULT 1046  
ID ABU19932 standard; protein; 396 AA.  
DE Protein encoded by prokaryotic essential gene #5459.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 72; DB 6; Length 396;  
Best Local Similarity 21.6%; Pred. No. 41;  
RESULT 1047  
ID ABG25051 standard; protein; 414 AA.  
DE Novel human diagnostic protein #25042.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.0%; Score 72; DB 4; Length 414;  
Best Local Similarity 22.6%; Pred. No. 44;  
RESULT 1048  
ID AAG50203 standard; protein; 427 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63592.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.0%; Score 72; DB 3; Length 427;  
Best Local Similarity 22.0%; Pred. No. 46;  
RESULT 1049  
ID AAG50202 standard; protein; 430 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63591.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.0%; Score 72; DB 3; Length 430;  
Best Local Similarity 22.0%; Pred. No. 46;  
RESULT 1050  
ID ABW72825 standard; protein; 447 AA.  
DE Staphylococcus aureus protein #2065.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.0%; Score 72; DB 6; Length 447;  
Best Local Similarity 23.9%; Pred. No. 49;  
RESULT 1051  
ID ABB62902 standard; protein; 448 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 15498.  
PN WO200177042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 6.0%; Score 72; DB 4; Length 448;  
Best Local Similarity 25.1%; Pred. No. 49;  
RESULT 1052  
ID AB118913 standard; protein; 453 AA.  
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 59.  
PN WO200259148-A2.  
PD 01-AUG-2002.  
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.  
Query Match 6.0%; Score 72; DB 6; Length 453;  
Best Local Similarity 23.9%; Pred. No. 50;  
RESULT 1053  
ID ABU16441 standard; protein; 453 AA.  
DE Protein encoded by prokaryotic essential gene #1968.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.0%; Score 72; DB 6; Length 453;  
Best Local Similarity 23.9%; Pred. No. 50;  
RESULT 1054  
ID ADN73057 standard; protein; 468 AA.  
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants Segid 952.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPPESIGN NV.  
Query Match 6.0%; Score 72; DB 8; Length 468;  
Best Local Similarity 21.8%; Pred. No. 52;  
RESULT 1055  
ID AAG16338 standard; protein; 495 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16945.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.0%; Score 72; DB 3; Length 495;  
Best Local Similarity 21.3%; Pred. No. 56;  
RESULT 1056  
ID AAC16337 standard; protein; 497 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16944.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (CHIR-) CHIRON SPA.  
Query Match 6.0%; Score 72; DB 3; Length 497;  
Best Local Similarity 21.3%; Pred. No. 57;

RESULT 1057  
ID AAG16336 standard; protein; 507 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16943.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 3; Length 507;  
21.3%; Pred. No. 58;  
RESULT 1058  
ID ADS23568 standard; protein; 543 AA.  
DE Bacterial polypeptide #12601.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 8; Length 543;  
18.6%; Pred. No. 64;  
RESULT 1059  
ID ARU25738 standard; protein; 552 AA.  
DE Protein encoded by Prokaryotic essential gene #11265.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 6; Length 552;  
19.5%; Pred. No. 65;  
RESULT 1060  
ID AAG50201 standard; protein; 556 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63590.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 3; Length 556;  
22.0%; Pred. No. 66;  
RESULT 1061  
ID ADJ69383 standard; protein; 594 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1189.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 7; Length 594;  
20.8%; Pred. No. 73;  
RESULT 1062  
ID ABP97202 standard; protein; 696 AA.  
DE Tumour-associated antigenic target protein TAR247 SEQ ID NO:84.  
PN WO2003024392-A2.  
PD 27-MAR-2003.  
PA (GETH-) GENENTECH INC.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 6; Length 696;  
20.8%; Pred. No. 90;  
RESULT 1063  
ID ABP97201 standard; protein; 696 AA.  
DE Tumour-associated antigenic target protein TAR225 SEQ ID NO:83.  
PN WO2003024392-A2.  
PD 27-MAR-2003.  
PA (GETH-) GENENTECH INC.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 6; Length 696;  
20.8%; Pred. No. 90;  
RESULT 1064  
ID ABP81969 standard; protein; 696 AA.  
DE Human GPCR XPR1 protein SEQ ID NO:424.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 6; Length 696;  
20.8%; Pred. No. 90;  
RESULT 1065  
ID ADB67652 standard; protein; 696 AA.  
DE Human xenotropic polytropic retrovirus receptor, SEQ ID 21.  
PN WO2003072824-A1.  
PD 04-SEP-2003.  
PA (SANY) SANKYO CO LTD.

Query Match  
Best Local Similarity 6.0%; Score 72; DB 7; Length 696;  
20.8%; Pred. No. 90;  
RESULT 1066  
ID AQO96380 standard; protein; 696 AA.  
DE T cell activation associated protein #279.  
PN WO2004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 8; Length 696;  
20.8%; Pred. No. 90;  
RESULT 1067  
ID ABM69179 standard; protein; 724 AA.  
DE Photorehabus luminescens protein sequence #2276.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (TNSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 6; Length 724;  
21.3%; Pred. No. 95;  
RESULT 1068  
ID AAB46702 standard; protein; 741 AA.  
DE P. falciparum DNA polymerase protein fragment SEQ ID NO 11.  
PN WO200075335-A2.  
PD 14-DEC-2000.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 4; Length 741;  
30.4%; Pred. No. 99;  
RESULT 1069  
ID AAM47977 standard; protein; 788 AA.  
DE Human hARG.  
PN CN1315342-A.  
PD 03-OCT-2001.  
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 5; Length 788;  
26.3%; Pred. No. 1.1e+02;  
RESULT 1070  
ID AAB56917 standard; protein; 1275 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 3543.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 4; Length 1275;  
19.0%; Pred. No. 2.1e+02;  
RESULT 1071  
ID AAY70064 standard; protein; 2307 AA.  
DE Recombinant fusion pHCAP-1 polypeptide.  
PN WO200008469-A1.  
PD 17-FEB-2000.  
PA (AGOU-) AGOURON PHARM INC.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 3; Length 2307;  
23.6%; Pred. No. 4.8e+02;  
RESULT 1072  
ID AAY70065 standard; protein; 2307 AA.  
DE Recombinant fusion pHCAP-3 polypeptide.  
PN WO200008469-A1.  
PD 17-FEB-2000.  
PA (AGOU-) AGOURON PHARM INC.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 3; Length 2307;  
23.6%; Pred. No. 4.8e+02;  
RESULT 1073  
ID AAY70066 standard; protein; 2307 AA.  
DE Recombinant fusion pHCAP-4 polypeptide.  
PN WO200008469-A1.  
PD 17-FEB-2000.  
PA (AGOU-) AGOURON PHARM INC.  
Query Match  
Best Local Similarity 6.0%; Score 72; DB 3; Length 2307;  
23.6%; Pred. No. 4.8e+02;  
RESULT 1074  
ID AAM93791 standard; protein; 208 AA.  
DE Human polypeptide, SEQ ID NO: 3817.  
PN EP1130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.



Query Match 6.0%; Score 71.5; DB 4; Length 208;  
Best Local Similarity 25.2%; Pred. No. 19;  
RESULT 1075  
ID ADL31784 standard; protein; 208 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 3817.  
PN EPI395543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 6.0%; Score 71.5; DB 8; Length 208;  
Best Local Similarity 25.2%; Pred. No. 19;  
RESULT 1076  
ID AAG56417 standard; protein; 209 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 72517.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 6.0%; Score 71.5; DB 3; Length 209;  
Best Local Similarity 25.6%; Pred. No. 19;  
RESULT 1077  
ID AAG56416 standard; protein; 216 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 72516.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 6.0%; Score 71.5; DB 3; Length 216;  
Best Local Similarity 25.6%; Pred. No. 20;  
RESULT 1078  
ID AAG16922 standard; protein; 218 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17750.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 6.0%; Score 71.5; DB 3; Length 218;  
Best Local Similarity 42.4%; Pred. No. 21;  
RESULT 1079  
ID ABB53486 standard; protein; 301 AA.  
DE Lactococcus lactis protein yb1G.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 6.0%; Score 71.5; DB 5; Length 301;  
Best Local Similarity 26.5%; Pred. No. 32;  
RESULT 1080  
ID AAM37976 standard; protein; 342 AA.  
DE Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.  
PN W09815289-A1.  
PD 16-APR-1998.  
PA (CORR-) CORNELL RES FOUND INC.  
Query Match 6.0%; Score 71.5; DB 2; Length 342;  
Best Local Similarity 22.2%; Pred. No. 39;  
RESULT 1081  
ID ADG87423 standard; protein; 348 AA.  
DE Meloidogyne incognita p1k1 protein.  
PN US2003150017-A1.  
PD 07-AUG-2003.  
PA (MESA/) MESA J R B.  
PA (GRAH/) GRAHAM M W.  
PA (FAIR/) FAIRBAIN D J.  
Query Match 6.0%; Score 71.5; DB 7; Length 348;  
Best Local Similarity 21.0%; Pred. No. 40;  
RESULT 1082  
ID ADR40542 standard; protein; 363 AA.  
DE Ovine ML1A protein.  
PN US2004161823-A1.  
PD 19-AUG-2004.  
PA (FEDE/) FEDER J N.  
PA (MINT/) MINTIER G.  
PA (RAMA/) RAMANATHAN C S.  
PA (HAWK/) HAWKEN D R.  
Query Match 6.0%; Score 71.5; DB 8; Length 363;  
Best Local Similarity 23.1%; Pred. No. 42;  
RESULT 1083  
ID AAR88410 standard; protein; 366 AA.  
DE High-affinity melatonin-1a receptor.  
PN W09535320-A1.  
PD 28-DEC-1995.  
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
Query Match 6.0%; Score 71.5; DB 2; Length 366;  
Best Local Similarity 23.1%; Pred. No. 42;  
RESULT 1084  
ID ABU03456 standard; protein; 382 AA.  
DE Angiogenesis-associated human protein sequence #1.  
PN W0200279492-A2.  
PD 10-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 45;  
RESULT 1085  
ID ABP58069 standard; protein; 382 AA.  
DE Human G-protein coupled receptor GAVEL.  
PN W0200295056-A2.  
PD 28-JUN-2002.  
PA (AVER-) AVENTIS PHARM INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 45;  
RESULT 1086  
ID ABP59277 standard; protein; 382 AA.  
DE Human Edg1 receptor.  
PN W02003006503-A1.  
PD 23-JAN-2003.  
PA (CERE-) CERETER.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 45;  
RESULT 1087  
ID ABU08809 standard; protein; 382 AA.  
DE Human EDG-1 protein.  
PN US2002155512-A1.  
PD 24-OCT-2002.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 45;  
RESULT 1088  
ID ABR59701 standard; protein; 382 AA.  
DE Human endothelial differentiation sphingolipid GPCR 1.  
PN W02003029277-A2.  
PD 10-APR-2003.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 45;  
RESULT 1089  
ID ABB81876 standard; protein; 382 AA.  
DE Human sphingolipid receptor Edg1 protein SEQ ID NO:237.  
PN W0200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 382;  
Best Local Similarity 22.3%; Pred. No. 45;  
RESULT 1090  
ID ADB67662 standard; protein; 382 AA.  
DE Human EDG1, SEQ ID 31.  
PN W02003072824-A1.  
PD 04-SEP-2003.  
PA (SANY) SANKYO CO LTD.  
Query Match 6.0%; Score 71.5; DB 7; Length 382;  
Best Local Similarity 22.3%; Pred. No. 45;  
RESULT 1091  
ID ADC40477 standard; protein; 382 AA.  
DE Protein of human EDG-1.  
PN W02003052096-A1.  
PD 26-JUN-2003.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 6.0%; Score 71.5; DB 7; Length 382;  
Best Local Similarity 22.3%; Pred. No. 45;  
RESULT 1092  
ID ADN38684 standard; protein; 382 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide. SEQ ID NO:2.  
PN W02003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.

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Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 382;
PRED. NO. 45;
RESULT 1093
ID ABM85457 standard; protein; 382 AA.
DE Human protein sequence hcp1630135.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGES DISCOVERY.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 382;
PRED. NO. 45;
RESULT 1094
ID ADJ45541 standard; protein; 382 AA.
DE LXR-ligand induced transcript seq id 72.
PN US2004023276-A1.
PD 05-FEB-2004.
PA (WARD/) WARD T R.
PA (MAOM/) MAO M.
PA (LINS/) LINSLEY P S.
PA (LUND/) LUND E.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 8; Length 382;
PRED. NO. 45;
RESULT 1095
ID ADR67022 standard; protein; 382 AA.
DE Human cancer associated protein sequence SEQ ID NO:68.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGES DISCOVERY INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 8; Length 382;
PRED. NO. 45;
RESULT 1096
ID ADY19566 standard; protein; 382 AA.
DE PRO polypeptide SEQ ID NO 5372.
PN WO2005016962-A2.
PD 24-FEB-2005.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 9; Length 382;
PRED. NO. 45;
RESULT 1097
ID ADZ12975 standard; protein; 382 AA.
DE Human cancer-associated protein #147.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR-) CHIRON CORP.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 9; Length 382;
PRED. NO. 45;
RESULT 1098
ID ADZ12973 standard; protein; 382 AA.
DE Human cancer-associated protein #146.
PN WO2005031001-A2.
PD 07-APR-2005.
PA (CHIR-) CHIRON CORP.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 9; Length 382;
PRED. NO. 45;
RESULT 1099
ID ADN19614 standard; protein; 383 AA.
DE Bacterial polypeptide #2267.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 8; Length 383;
PRED. NO. 45;
RESULT 1100
ID ABB05226 standard; protein; 390 AA.
DE Gatoctonus comarsoni isotocin receptor protein SEQ ID NO:3.
PN WO200192296-A2.
PD 06-DEC-2001.
PA (PARB-) BAYER AG.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 5; Length 390;
PRED. NO. 46;
RESULT 1101
ID ADM83141 standard; protein; 394 AA.
DE Rat vesicle membrane protein (VMP)2.
PN US2003175787-A1.
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 394;
PRED. NO. 47;
RESULT 1102
ID ABB48023 standard; protein; 435 AA.
DE Listeria monocytogenes protein #727.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTEUR.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 5; Length 435;
PRED. NO. 54;
RESULT 1103
ID AAR22000 standard; protein; 441 AA.
DE Partial M17 antigen from Region II, encoded by PCR prod.
PN WO9203457-A.
PD 05-MAR-1992.
PA (REGC-) UNIV CALIFORNIA.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 2; Length 441;
PRED. NO. 55;
RESULT 1104
ID ADX93096 standard; protein; 448 AA.
DE Plant full length insert polypeptide seqid 55760.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 8; Length 448;
PRED. NO. 56;
RESULT 1105
ID ABB75877 standard; protein; 470 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1061.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 470;
PRED. NO. 60;
RESULT 1106
ID ABU26033 standard; protein; 524 AA.
DE Protein encoded by Prokaryotic essential gene #11560.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 524;
PRED. NO. 70;
RESULT 1107
ID ABJ37074 standard; protein; 565 AA.
DE Human breast cancer / ovarian cancer related protein #50.
PN WO2003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 565;
PRED. NO. 77;
RESULT 1108
ID AAW51244 standard; protein; 568 AA.
DE Human calcitonin receptor.
PN WO9821242-A1.
PD 22-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 2; Length 568;
PRED. NO. 78;
RESULT 1109
ID ABU16392 standard; protein; 603 AA.
DE Protein encoded by Prokaryotic essential gene #1919.
PN WO200277183-A2.
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PD 03-OCT-2002.
PA (ELIT-) ELITPA PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 603;
Best Local Similarity 21.3%; Pred. No. 85;
RESULT 1110
ID ABB72619 standard; protein; 603 AA.
DE Staphylococcus aureus protein #1859.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.0%; Score 71.5; DB 6; Length 603;
Best Local Similarity 21.3%; Pred. No. 85;
RESULT 1111
ID ADM43215 standard; protein; 697 AA.
DE Human methionine synthase reductase del Arg 559 variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 1e+02;
RESULT 1112
ID ADM43217 standard; protein; 697 AA.
DE Human methionine synthase reductase del Leu 576 variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 1e+02;
RESULT 1113
ID AAB07591 standard; protein; 698 AA.
DE A human methionine synthase reductase polypeptide.
PN WO2004042196-A2.
PD 20-JUL-2000.
PA (UYMC-) UNIV MCGILL.
Query Match 6.0%; Score 71.5; DB 3; Length 698;
Best Local Similarity 22.8%; Pred. No. 1e+02;
RESULT 1114
ID ABG00883 standard; protein; 698 AA.
DE Novel human diagnostic protein #874.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 71.5; DB 4; Length 698;
Best Local Similarity 22.8%; Pred. No. 1e+02;
RESULT 1115
ID ADM43211 standard; protein; 698 AA.
DE Human methionine synthase reductase Met2211e variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 1e+02;
RESULT 1116
ID ADM43213 standard; protein; 698 AA.
DE Human methionine synthase reductase Cys377Yr variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 1e+02;
RESULT 1117
ID ADM43207 standard; protein; 698 AA.
DE Human wild-type methionine synthase reductase.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 1e+02;
RESULT 1118
ID ADQ39857 standard; protein; 698 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1520.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 71.5; DB 8; Length 698;
Best Local Similarity 22.8%; Pred. No. 1e+02;
RESULT 1119
ID ADQ39858 standard; protein; 725 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1521.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 71.5; DB 8; Length 725;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1120
ID ADU06586 standard; protein; 725 AA.
DE Novel bronchial cancer-associated human protein SeqID812.
PN DE10316701-A1.
PD 04-NOV-2004.
PA (HINZ/) HINZMANN B.
PA (HERM/) HERMANN K.
PA (CAST/) HEIDEN CASTANOS-VELEZ E.
Query Match 6.0%; Score 71.5; DB 8; Length 725;
Best Local Similarity 22.8%; Pred. No. 1.1e+02;
RESULT 1121
ID AAY51606 standard; protein; 890 AA.
DE Human wml protein.
PN DE19845277-C1.
PD 09-MAR-2000.
PA (UYMU-) UNIV MUEENCHEN MAXIMILIANS LUDWIG.
Query Match 6.0%; Score 71.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.5e+02;
RESULT 1122
ID ABB78282 standard; protein; 890 AA.
DE Amino acid sequence of human wolframin polypeptide.
PN WO200263307-A2.
PD 15-AUG-2002.
PA (PHAA-) PHARMACIA & UPJOHN CO.
Query Match 6.0%; Score 71.5; DB 5; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.5e+02;
RESULT 1123
ID ADD46013 standard; protein; 890 AA.
DE Human Protein 076024, SEQ ID NO 11685.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 6.0%; Score 71.5; DB 7; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.5e+02;
RESULT 1124
ID ADF69127 standard; protein; 890 AA.
DE Human MP53 protein sequence SEQ ID NO:97.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match 6.0%; Score 71.5; DB 7; Length 890;
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Best Local Similarity 23.8%; Pred. No. 1.5e+02;  
RESULT 1125  
ID ADY70426 standard; protein; 890 AA.  
DE Human beta-amyloid precursor protein, wolframin.  
PN WO2005023858-A1.  
PD 17-MAR-2005.  
PA (CELL-) CELLZOME AG.  
Query Match 6.0%; Score 71.5; DB 9; Length 890;  
Best Local Similarity 23.8%; Pred. No. 1.5e+02;  
RESULT 1126  
ID ADY70680 standard; protein; 890 AA.  
DE Human nilecastrin/Psen2-complex member, wolframin protein.  
PN WO2005023833-A2.  
PD 17-MAR-2005.  
PA (CELL-) CELLZOME AG.  
Query Match 6.0%; Score 71.5; DB 9; Length 890;  
Best Local Similarity 23.8%; Pred. No. 1.5e+02;  
RESULT 1127  
ID ADL22689 standard; protein; 2245 AA.  
DE Human disease detection and treatment (MDPT) protein - SEQ ID 138.  
PN WO2003063379-A2.  
PD 31-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.0%; Score 71.5; DB 7; Length 2245;  
Best Local Similarity 22.4%; Pred. No. 5.2e+02;  
RESULT 1128  
ID ABA42192 standard; protein; 2405 AA.  
DE Human ORFX ORF1956 polypeptide sequence SEQ ID NO:3912.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 6.0%; Score 71.5; DB 3; Length 2405;  
Best Local Similarity 22.4%; Pred. No. 5.8e+02;  
RESULT 1129  
ID ABB11404 standard; peptide; 2560 AA.  
DE Human FLAMINGO 1 homologue, SEQ ID NO:1774.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 6.0%; Score 71.5; DB 4; Length 2560;  
Best Local Similarity 22.4%; Pred. No. 6.3e+02;  
RESULT 1130  
ID ABB11556 standard; protein; 2894 AA.  
DE Human MDP1 polypeptide SEQ ID 503.  
PN WO200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 2894;  
Best Local Similarity 22.4%; Pred. No. 7.5e+02;  
RESULT 1131  
ID AAU07054 standard; protein; 2923 AA.  
DE Human Flamingo protein encoded by cDNA splice variant.  
PN WO200161003-A1.  
PD 23-AUG-2001.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 6.0%; Score 71.5; DB 4; Length 2923;  
Best Local Similarity 22.4%; Pred. No. 7.6e+02;  
RESULT 1132  
ID AAM50866 standard; protein; 2923 AA.  
DE Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.  
PN WO200208765-A2.  
PD 31-JAN-2002.  
PA (STRD) UNIV STANFORD.  
Query Match 6.0%; Score 71.5; DB 5; Length 2923;  
Best Local Similarity 22.4%; Pred. No. 7.6e+02;  
RESULT 1133  
ID ABB82018 standard; protein; 2923 AA.  
DE Human BACE1/PTK7-complex member, CELSR2 protein.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 6.0%; Score 71.5; DB 6; Length 2923;

Best Local Similarity 22.4%; Pred. No. 7.6e+02;  
RESULT 1134  
ID ADC15499 standard; protein; 2923 AA.  
DE Human cadherin EGF LAG seven-pass G-type receptor 2.  
PN US2003086934-A1.  
PD 08-MAY-2003.  
PA (BOTS/) BOTSTEIN D.  
PA (BROW/) BROWN P O.  
PA (PERO/) PEROU C M.  
PA (RING/) RING B.  
PA (ROSS/) ROSS D.  
PA (SEIT/) SEITZ R.  
PA (VRID/) VAN DE RIJN J M.  
Query Match 6.0%; Score 71.5; DB 7; Length 2923;  
Best Local Similarity 22.4%; Pred. No. 7.6e+02;  
RESULT 1135  
ID ADC86479 standard; protein; 2923 AA.  
DE Human GPCR protein SEQ ID NO:932.  
PN EP1270724-A2.  
PD 02-JAN-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Query Match 6.0%; Score 71.5; DB 7; Length 2923;  
Best Local Similarity 22.4%; Pred. No. 7.6e+02;  
RESULT 1136  
ID ADE54407 standard; protein; 2923 AA.  
DE Human Protein XP\_042739, SEQ ID NO 210.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 6.0%; Score 71.5; DB 7; Length 2923;  
Best Local Similarity 22.4%; Pred. No. 7.6e+02;  
RESULT 1137  
ID ADE54411 standard; protein; 2923 AA.  
DE Human Protein XP\_042739, SEQ ID NO 214.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 6.0%; Score 71.5; DB 7; Length 2923;  
Best Local Similarity 22.4%; Pred. No. 7.6e+02;  
RESULT 1138  
ID ADO29245 standard; protein; 2923 AA.  
DE Human GPCR CELSR2, SEQ ID NO:346.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 6.0%; Score 71.5; DB 8; Length 2923;  
Best Local Similarity 22.4%; Pred. No. 7.6e+02;  
RESULT 1139  
ID ADY70314 standard; protein; 2923 AA.  
DE Human beta-APP, cadherin EGF LAG seven-pass G-type receptor 2.  
PN WO2005023858-A1.  
PD 17-MAR-2005.  
PA (CELL-) CELLZOME AG.  
Query Match 6.0%; Score 71.5; DB 9; Length 2923;  
Best Local Similarity 22.4%; Pred. No. 7.6e+02;  
RESULT 1140  
ID ADY70652 standard; protein; 2923 AA.  
DE Human BACE1/PTK7-complex member, CELSR2 protein.  
PN WO2005023833-A2.  
PD 17-MAR-2005.  
PA (CELL-) CELLZOME AG.  
Query Match 6.0%; Score 71.5; DB 9; Length 2923;  
Best Local Similarity 22.4%; Pred. No. 7.6e+02;  
RESULT 1141  
ID ADY70648 standard; protein; 2923 AA.  
DE Human BACE1-complex, cadherin seven-pass G-type receptor 2 protein.  
PN WO2005023833-A2.  
PD 17-MAR-2005.  
PA (CELL-) CELLZOME AG.  
Query Match 6.0%; Score 71.5; DB 9; Length 2923;

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Best Local Similarity 22.4%; Pred. No. 7.6e+02;
RESULT 1142
ID AAU74826 standard; protein; 2936 AA.
DE Human REPR 9 protein.
PN WO200198354-A2.
PD 27-DEC-2001.
PA (INCYTE-) INCYTE GENOMICS INC.
Query Match 6.0%; Score 71.5; DB 5; Length 2936;
Best Local Similarity 22.4%; Pred. No. 7.6e+02;
RESULT 1143
ID AAU07053 standard; protein; 2956 AA.
DE Human Flamingo polypeptide.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIK-) SMITHKLINE BEECHAM PLC.
Query Match 6.0%; Score 71.5; DB 4; Length 2956;
Best Local Similarity 22.4%; Pred. No. 7.7e+02;
RESULT 1144
ID ADX40788 standard; protein; 3010 AA.
DE HCV polymerase protein #11.
PN WO2005012502-A2.
PD 10-FEB-2005.
PA (EPIM-) EPIMUNE INC.
Query Match 6.0%; Score 71.5; DB 9; Length 3010;
Best Local Similarity 23.7%; Pred. No. 7.9e+02;
RESULT 1145
ID AAR34468 standard; protein; 3011 AA.
DE Encoded by full-length Hepatitis C virus clone JKI-B.
PN JP05068562-A.
PD 23-MAR-1993.
PA (SANM-) SANMA KAGAKU KENKYUSHO CO.
Query Match 6.0%; Score 71.5; DB 2; Length 3011;
Best Local Similarity 23.7%; Pred. No. 7.9e+02;
RESULT 1146
ID AAR31621 standard; protein; 3011 AA.
DE Hepatitis C virus (HCV) polypeptide.
PN WO9300365-A2.
PD 07-JAN-1993.
PA (CHIR-) CHIRON CORP.
Query Match 6.0%; Score 71.5; DB 2; Length 3011;
Best Local Similarity 22.8%; Pred. No. 7.9e+02;
RESULT 1147
ID ABB6766 standard; protein; 5303 AA.
DE Diosophila melanogaster polypeptide SEQ ID NO 30390.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.0%; Score 71.5; DB 4; Length 5303;
Best Local Similarity 29.5%; Pred. No. 1.7e+03;
RESULT 1148
ID ABB06793 standard; protein; 198 AA.
DE Human transmembrane 4 protein 22 SEQ ID NO:2.
PN CN1327990-A.
PD 26-DEC-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 5.9%; Score 71; DB 5; Length 198;
Best Local Similarity 24.5%; Pred. No. 21;
RESULT 1149
ID ADU08919 standard; protein; 223 AA.
DE Coronavirus membrane protein seqid 42.
PN WO2004096842-A2.
PD 11-NOV-2004.
PA (BCCA-) BC CANCER AGENCY.
Query Match 5.9%; Score 71; DB 8; Length 223;
Best Local Similarity 22.4%; Pred. No. 24;
RESULT 1150
ID ABR58398 standard; protein; 240 AA.
DE Human NOV17a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 71; DB 6; Length 240;
Best Local Similarity 18.6%; Pred. No. 27;

RESULT 1151
ID ABB26255 standard; protein; 295 AA.
DE Streptococcus polypeptide SEQ ID NO 1686.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.9%; Score 71; DB 5; Length 295;
Best Local Similarity 24.9%; Pred. No. 36;
RESULT 1152
ID ADX65958 standard; protein; 309 AA.
DE Plant full length insert polypeptide seqid 36801.
PN US200403488-A1.
PD 19-FEB-2004.
PA (LIUJ-) LIU J.
PA (ZHOU-) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CHOY/) CAO Y.
Query Match 5.9%; Score 71; DB 8; Length 309;
Best Local Similarity 18.7%; Pred. No. 38;
RESULT 1153
ID AAG72952 standard; protein; 310 AA.
DE Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA-) YEDA RES & DEV CO LTD.
Query Match 5.9%; Score 71; DB 4; Length 310;
Best Local Similarity 22.9%; Pred. No. 39;
RESULT 1154
ID AAR48717 standard; protein; 312 AA.
DE G-protein coupled human Interleukin-8 receptor protein.
PN WO9405695-A1.
PD 17-MAR-1994.
PA (UVNY) UNIV NEW YORK STATE.
Query Match 5.9%; Score 71; DB 2; Length 312;
Best Local Similarity 19.7%; Pred. No. 39;
RESULT 1155
ID AAW02689 standard; peptide; 312 AA.
DE G-protein coupled human Interleukin-8 receptor.
PN US5508384-A.
PD 16-APR-1996.
PA (UVNY) UNIV NEW YORK STATE.
Query Match 5.9%; Score 71; DB 2; Length 312;
Best Local Similarity 19.7%; Pred. No. 39;
RESULT 1156
ID AAG72169 standard; protein; 312 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1850.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA-) YEDA RES & DEV CO LTD.
Query Match 5.9%; Score 71; DB 4; Length 312;
Best Local Similarity 22.9%; Pred. No. 39;
RESULT 1157
ID AAG72377 standard; protein; 312 AA.
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2058.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA-) YEDA RES & DEV CO LTD.
Query Match 5.9%; Score 71; DB 4; Length 312;
Best Local Similarity 22.9%; Pred. No. 39;
RESULT 1158
ID ADV08080 standard; protein; 364 AA.
DE Plant full length insert polypeptide seqid 63895.
PN US200403488-A1.
PD 19-FEB-2004.
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
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PA (SCREEN) SCREEN S.E.  
PA (TAB) TABASKA J.E.  
PA (CAOY) CAO Y.  
Query Match 5.9%; Score 71; DB 8; Length 364;  
Best Local Similarity 18.7%; Pred. No. 48;  
RESULT 1159  
ID ABB54394 standard; protein; 391 AA.  
DE Lactococcus lactis protein ykii.  
PN PR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 5.9%; Score 71; DB 5; Length 391;  
Best Local Similarity 20.3%; Pred. No. 53;  
RESULT 1160  
ID ABB48413 standard; protein; 423 AA.  
DE Listeria monocytogenes protein #1117.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP) INST PASTEUR.  
Query Match 5.9%; Score 71; DB 5; Length 423;  
Best Local Similarity 28.4%; Pred. No. 59;  
RESULT 1161  
ID ADL05302 standard; protein; 423 AA.  
DE M. catarrhalis protein #1068.  
PN US6673910-B1.  
PD 06-JAN-2004.  
PA (GENO) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 71; DB 8; Length 423;  
Best Local Similarity 38.0%; Pred. No. 59;  
RESULT 1162  
ID ADJ95142 standard; protein; 444 AA.  
DE Novel NOVX protein sequence #185.  
PN WO2003040325-A2.  
PD 15-MAY-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.9%; Score 71; DB 7; Length 444;  
Best Local Similarity 21.0%; Pred. No. 63;  
RESULT 1163  
ID ADJ95144 standard; protein; 444 AA.  
DE Novel NOVX protein sequence #186.  
PN WO2003040325-A2.  
PD 15-MAY-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.9%; Score 71; DB 7; Length 444;  
Best Local Similarity 21.0%; Pred. No. 63;  
RESULT 1164  
ID ADU73808 standard; protein; 448 AA.  
DE Drosophila melanogaster Cbl-D.  
PN WO2004099388-A2.  
PD 18-NOV-2004.  
PA (PROT-) PROTEOLOGICS INC.  
Query Match 5.9%; Score 71; DB 8; Length 448;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 1165  
ID ADU69155 standard; protein; 448 AA.  
DE Fruit fly Cbl-B protein.  
PN WO2004098492-A2.  
PD 18-NOV-2004.  
PA (PROT-) PROTEOLOGICS INC.  
Query Match 5.9%; Score 71; DB 8; Length 448;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 1166  
ID ADM87442 standard; protein; 448 AA.  
DE Drosophila melanogaster Cbl-B.  
PN WO2005007141-A2.  
PD 27-JAN-2005.  
PA (PROT-) PROTEOLOGICS INC.  
Query Match 5.9%; Score 71; DB 9; Length 448;  
Best Local Similarity 23.5%; Pred. No. 64;  
RESULT 1167  
ID ADP29417 standard; protein; 455 AA.  
DE Human secreted protein SEQ ID #184.  
PN WO2004035732-A2.

PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 5.9%; Score 71; DB 8; Length 455;  
Best Local Similarity 24.3%; Pred. No. 66;  
RESULT 1168  
ID ABU19912 standard; protein; 457 AA.  
DE Protein encoded by Prokaryotic essential gene #5439.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 71; DB 6; Length 457;  
Best Local Similarity 22.0%; Pred. No. 66;  
RESULT 1169  
ID ADI24575 standard; protein; 470 AA.  
DE Human endogenous 5HT2A serotonin receptor.  
PN US2003224442-A1.  
PD 04-DEC-2003.  
PA (BEHA/) BEHAN D.P.  
PA (CHAL/) CHALMERS D.T.  
PA (LIAM/) LIAM C.W.  
PA (RUSO/) RUSSO J.F.  
PA (THOM/) THOMSEN W.J.  
Query Match 5.9%; Score 71; DB 8; Length 470;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1170  
ID AAR37659 standard; protein; 471 AA.  
DE Sequence encoded by cDNA.  
PN WO9311257-A2.  
PD 10-JUN-1993.  
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.  
Query Match 5.9%; Score 71; DB 2; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1171  
ID AAW23781 standard; protein; 471 AA.  
DE Human serotonin 5-HT2 receptor protein.  
PN US5661024-A.  
PD 26-AUG-1997.  
PA (SYNA-) SYNAPTIC PHARM CORP.  
Query Match 5.9%; Score 71; DB 2; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1172  
ID AAW77107 standard; protein; 471 AA.  
DE Human 5-HT2A serotonin receptor.  
PN WO9838217-A1.  
PD 03-SEP-1998.  
PA (TEIT/) TEITLER M.  
PA (HERR/) HERRICK-DAVIS K.  
PA (EGAN/) EGAN C.C.  
Query Match 5.9%; Score 71; DB 2; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1173  
ID AAY90640 standard; protein; 471 AA.  
DE Human G protein-coupled receptor 5HT-2A (serotonin receptor).  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 71; DB 3; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1174  
ID AAY90675 standard; protein; 471 AA.  
DE Human mutant G protein-coupled receptor 5HT-2A.  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 71; DB 3; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1175  
ID ABB07978 standard; protein; 471 AA.  
DE Human 5-HT2 receptor sequence.  
PN US6383763-B1.  
PD 07-MAY-2002.  
PA (SYNA-) SYNAPTIC PHARM CORP.  
Query Match 5.9%; Score 71; DB 5; Length 471;

Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1176  
ID ABB81765 standard; protein; 471 AA.  
DE Human 5-HT2A receptor protein SEQ ID NO:12.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 5.9%; Score 71; DB 6; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1177  
ID ADC22641 standard; protein; 471 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #32.  
PN US6555339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1178  
ID ADC22747 standard; protein; 471 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #72.  
PN US6555339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1179  
ID ADE65844 standard; protein; 471 AA.  
DE Human serotonin 2A receptor.  
PN US2003170723-A1.  
PD 11-SEP-2003.  
PA (SATO/) SATO T.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1180  
ID ADH14220 standard; protein; 471 AA.  
DE Mutated human serotonin 5HT\_2A.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAM/) LIAM C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1181  
ID ADH14114 standard; protein; 471 AA.  
DE Human serotonin 5HT\_2A.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAM/) LIAM C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1182  
ID ADJ90125 standard; protein; 471 AA.  
DE Human serotonin receptor 5HT2a.  
PN US2003167476-A1.  
PD 04-SEP-2003.  
PA (CONK/) CONKIN B R.  
Query Match 5.9%; Score 71; DB 7; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1183  
ID ADO29506 standard; protein; 471 AA.  
DE Human GPCR HTR2A, SEQ ID NO:608.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMM INC.  
Query Match 5.9%; Score 71; DB 8; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1184  
ID ADO39800 standard; protein; 471 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1463.  
PN WO2004058052-A2.

PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 5.9%; Score 71; DB 8; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1185  
ID ADO39799 standard; protein; 471 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1462.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 5.9%; Score 71; DB 8; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1186  
ID ADO39798 standard; protein; 471 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1461.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 5.9%; Score 71; DB 8; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1187  
ID ADU48367 standard; protein; 471 AA.  
DE Human serotonin 2A receptor protein.  
PN US2004232927-A1.  
PD 18-NOV-2004.  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
Query Match 5.9%; Score 71; DB 8; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1188  
ID ADX02782 standard; protein; 471 AA.  
DE Human 5-HT 2a receptor protein SeqID22.  
PN WO2005012254-A1.  
PD 10-FEB-2005.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 71; DB 9; Length 471;  
Best Local Similarity 23.7%; Pred. No. 69;  
RESULT 1189  
ID AAY01626 standard; protein; 478 AA.  
DE Amino acid sequence of the human 5-HT2 receptor.  
PN US5885785-A.  
PD 23-MAR-1999.  
PA (SYNA-) SYNAPTIC PHARM CORP.  
Query Match 5.9%; Score 71; DB 2; Length 478;  
Best Local Similarity 23.7%; Pred. No. 70;  
RESULT 1190  
ID ABG70577 standard; protein; 480 AA.  
DE Human serotonin (5-HT2) receptor.  
PN US2002098548-A1.  
PD 25-JUL-2002.  
PA (SYNA-) SYNAPTIC PHARM CORP.  
Query Match 5.9%; Score 71; DB 5; Length 480;  
Best Local Similarity 23.7%; Pred. No. 71;  
RESULT 1191  
ID ABW70440 standard; protein; 493 AA.  
DE Photorehabdus luminescens protein sequence #3537.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 71; DB 6; Length 493;  
Best Local Similarity 23.5%; Pred. No. 73;  
RESULT 1192  
ID ADE56383 standard; protein; 545 AA.  
DE Rat Protein O70536, SEQ ID NO 2235.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 5.9%; Score 71; DB 7; Length 545;  
Best Local Similarity 22.0%; Pred. No. 84;  
RESULT 1193  
ID ADD4660 standard; protein; 545 AA.  
DE Rat Protein BAA25372, SEQ ID NO 14366.

PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (PARB ) BAYER AG.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 7; Length 545;  
RESULT 1194  
ID ADS43584 standard; protein; 546 AA.  
DE Bacterial polypeptide #22014.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 8; Length 546;  
RESULT 1195  
ID ABJ26399 standard; protein; 559 AA.  
DE Aspergillus fumigatus essential gene protein #1057.  
PN W0200286690-A2.  
PD 31-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 6; Length 559;  
RESULT 1196  
ID ABP35686 standard; protein; 563 AA.  
DE Fungal ZEC protein sequence #112.  
PN W0200224865-A2.  
PD 28-MAR-2002.  
PA (MICR-) MICROBIA INC.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 5; Length 563;  
RESULT 1197  
ID AAB20578 standard; protein; 564 AA.  
DE Mouse OCTN3 protein SEQ ID NO:1.  
PN W0200046368-A1.  
PD 10-AUG-2000.  
PA (CHUC-) CHUCAI RES INST MOLECULAR MEDICINE INC.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 3; Length 564;  
RESULT 1198  
ID AEB36506 standard; protein; 603 AA.  
DE L. pneumophila protein SEQ ID NO 838.  
PN W02005048642-A2.  
PD 02-JUN-2005.  
PA (INSP ) INST PASTEUR.  
PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 9; Length 603;  
RESULT 1199  
ID ADQ96374 standard; protein; 631 AA.  
DE T cell activation associated protein #276.  
PN W02004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAHAI KASEI PHARMA CORP.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 8; Length 631;  
RESULT 1200  
ID ADQ96376 standard; protein; 631 AA.  
DE T cell activation associated protein #277.  
PN W02004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAHAI KASEI PHARMA CORP.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 8; Length 631;  
RESULT 1201  
ID ABB91532 standard; protein; 676 AA.  
DE Herbicidally active polypeptide SEQ ID NO 743.  
PN W0200210210-A2.

PD 07-FEB-2002.  
PA (PARB ) BAYER AG.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 5; Length 676;  
RESULT 1202  
ID AAE21800 standard; protein; 727 AA.  
DE Human HIPHUM 0000029 protein.  
PN GB2365432-A.  
PD 20-FEB-2002.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 5; Length 727;  
RESULT 1203  
ID ABUS4636 standard; protein; 727 AA.  
DE Human NOVX polypeptide #95.  
PN W0200281498-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 6; Length 727;  
RESULT 1204  
ID ADH76500 standard; protein; 727 AA.  
DE 727 amino acid human neurotransmitter transporter protein.  
PN US2003219774-A1.  
PD 27-NOV-2003.  
PA (SHAR/) SHARMA R.  
PA (RAMA/) RAMANATHAN C S.  
PA (WEST/) WESTPHAL R.  
PA (FEDE/) FEDER J N.  
PA (LEEL/) LEE L M.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 8; Length 727;  
RESULT 1205  
ID ABR62929 standard; protein; 744 AA.  
DE Human neurotransmitter transporter.  
PN W02003059947-A1.  
PD 24-JUL-2003.  
PA (PARB ) BAYER AG.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 7; Length 744;  
RESULT 1206  
ID ABB60052 standard; protein; 792 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 6948.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKS ) PE CORP NY.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 4; Length 792;  
RESULT 1207  
ID AAM90462 standard; protein; 929 AA.  
DE Rice abiotic stress responsive polypeptide SEQ ID NO:9184.  
PN W02003008540-A2.  
PD 30-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 7; Length 929;  
RESULT 1208  
ID AAR30616 standard; protein; 3010 AA.  
DE Polypeptide coded by Korean HCV full cDNA sequence LBCL.  
PN EP521318-A2.  
PD 07-JAN-1993.  
PA (LUCK-) LUCKY LTD.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 2; Length 3010;  
RESULT 1209  
ID AAR33417 standard; protein; 3010 AA.  
DE Blood transmissible NANBHV protein.  
PN JP06105690-A.  
PD 19-APR-1994.  
PA (KAEN/) KAENNO K.  
Query Match  
Best Local Similarity 5.9%; Score 71; DB 2; Length 3010;  
RESULT 1210  
ID ABB91532 standard; protein; 676 AA.  
DE Herbicidally active polypeptide SEQ ID NO 743.  
PN W0200210210-A2.



ID ADX40817 standard; protein; 3010 AA.  
DE HCV polymerase protein #40.  
PN WO2005012502-A2.  
PD 10-FEB-2005.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 5.9%; Score 71; DB 9; Length 3010;  
Best Local Similarity 26.9%; Pred. No. 9e+02;  
RESULT 1211  
ID ADX40783 standard; protein; 3010 AA.  
DE HCV polymerase protein #6.  
PN WO2005012502-A2.  
PD 10-FEB-2005.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 5.9%; Score 71; DB 9; Length 3010;  
Best Local Similarity 26.9%; Pred. No. 9e+02;  
RESULT 1212  
ID ADX40812 standard; protein; 3010 AA.  
DE HCV polymerase protein #35.  
PN WO2005012502-A2.  
PD 10-FEB-2005.  
PA (EPIM-) EPIMMUNE INC.  
Query Match 5.9%; Score 71; DB 9; Length 3010;  
Best Local Similarity 26.9%; Pred. No. 9e+02;  
RESULT 1213  
ID ABR83573 standard; protein; 202 AA.  
DE Bcfc amino acid sequence SEQ ID NO:40.  
PN WO2003057708-A2.  
PD 17-JUL-2003.  
PA (UYNE-) UNIV NEWCASTLE VENTURES LTD.  
Query Match 5.9%; Score 70.5; DB 6; Length 202;  
Best Local Similarity 26.5%; Pred. No. 24;  
RESULT 1214  
ID AAU01287 standard; protein; 218 AA.  
DE Brassica napus fatty acid desaturase, Fad3c, partial sequence.  
PN WO200125453-A2.  
PD 12-APR-2001.  
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
Query Match 5.9%; Score 70.5; DB 4; Length 218;  
Best Local Similarity 29.3%; Pred. No. 27;  
RESULT 1215  
ID AAU97208 standard; protein; 228 AA.  
DE Portion of a wheat sugar transport protein encoded by wreln.pk0006.b4.  
PN US6383776-B1.  
PD 07-MAY-2002.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 5.9%; Score 70.5; DB 5; Length 228;  
Best Local Similarity 21.6%; Pred. No. 29;  
RESULT 1216  
ID ABU08333 standard; protein; 228 AA.  
DE Wheat sugar transport protein #3.  
PN US2002178468-A1.  
PD 28-NOV-2002.  
PA (ALLE/) ALLEN S M.  
PA (HITZ/) HITZ W D.  
PA (KINN/) KINNEY A J.  
PA (TING/) TINGEY S V.  
Query Match 5.9%; Score 70.5; DB 6; Length 228;  
Best Local Similarity 21.6%; Pred. No. 29;  
RESULT 1217  
ID ADG47920 standard; protein; 228 AA.  
DE Wheat Arabidopsis-like sugar transport protein #3.  
PN US2002199217-A1.  
PD 26-DEC-2002.  
PA (HELE/) HELENTJARIS T G.  
Query Match 5.9%; Score 70.5; DB 8; Length 228;  
Best Local Similarity 21.6%; Pred. No. 29;  
RESULT 1218  
ID ABU17430 standard; protein; 275 AA.  
DE Protein encoded by Prokaryotic essential gene #2957.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 70.5; DB 6; Length 275;

Best Local Similarity 22.8%; Pred. No. 37;  
RESULT 1219  
ID ADY06253 standard; protein; 283 AA.  
DE Plant full length insert polypeptide seqid 62068.  
PN US2004034888-A1.  
PD 19-FEB-2004.  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABA/) TABASKA J E.  
PA (CAOY/) CAO Y.  
Query Match 5.9%; Score 70.5; DB 8; Length 283;  
Best Local Similarity 27.4%; Pred. No. 39;  
RESULT 1220  
ID ABB55033 standard; protein; 285 AA.  
DE Lactococcus lactis protein malG.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 5.9%; Score 70.5; DB 5; Length 285;  
Best Local Similarity 26.1%; Pred. No. 39;  
RESULT 1221  
ID ABB05467 standard; protein; 291 AA.  
DE Coriolus versicolor aldo/ketoreductase protein SEQ ID NO:2.  
PN JP2001321171-A.  
PD 20-NOV-2001.  
PA (WARI/) WARIISHI H.  
PA (KUBI) KUBOTA CORP.  
Query Match 5.9%; Score 70.5; DB 5; Length 291;  
Best Local Similarity 29.4%; Pred. No. 40;  
RESULT 1222  
ID ADA35787 standard; protein; 297 AA.  
DE Acinetobacter baumannii protein #2948.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 70.5; DB 6; Length 297;  
Best Local Similarity 24.1%; Pred. No. 42;  
RESULT 1223  
ID ABEW70358 standard; protein; 321 AA.  
DE Photorhabdus luminescens protein sequence #3455.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70.5; DB 6; Length 321;  
Best Local Similarity 19.2%; Pred. No. 46;  
RESULT 1224  
ID ADH22355 standard; protein; 330 AA.  
DE Human receptor & membrane associated protein (REMAP) SeqIDS.  
PN WO2003104395-A2.  
PD 18-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 5.9%; Score 70.5; DB 8; Length 330;  
Best Local Similarity 24.2%; Pred. No. 48;  
RESULT 1225  
ID ADK68232 standard; protein; 343 AA.  
DE Novel NOVX protein #79.  
PN WO2003085124-A2.  
PD 16-OCT-2003.  
PA (CURA-) CURAEN CORP.  
Query Match 5.9%; Score 70.5; DB 7; Length 343;  
Best Local Similarity 30.0%; Pred. No. 51;  
RESULT 1226  
ID ADH72226 standard; protein; 343 AA.  
DE Human protein of the invention NOV55a SEQ ID NO:1122.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAEN CORP.  
Query Match 5.9%; Score 70.5; DB 8; Length 343;  
Best Local Similarity 30.0%; Pred. No. 51;  
RESULT 1227

ID ADR49221 standard; protein; 343 AA.  
DE Human NOV10a protein.  
PN US2004162236-A1.  
PD 19-AUG-2004  
PA (ALSO) ALSOBROOK J.  
PA (BENT) BENTO P.  
PA (BOLD) BOLDG F.  
PA (BURG) BURGESS C.  
PA (CASM) CASMAN S.  
PA (BOKO) BOKOR J C.  
PA (EDIN) EDINGER S R.  
PA (ELLE) ELLERMAN K.  
PA (FERN) FERNANDES E.  
PA (GERL) GERLACH V.  
PA (GROS) GROSSE W.  
PA (GUNT) GUNTHER E.  
PA (GUSE) GUSEV V.  
PA (HEYE) HEYES M.  
PA (LEPL) LEPLEY D.  
PA (LILL) LI L.  
PA (MACD) MACDOUGALL J R.  
PA (MALY) MALYANKAR U M.  
PA (MILL) MILLET I.  
PA (PAT) PATURAJAN M.  
PA (PEYM) PEYMAN J A.  
PA (RAST) RASTELLI L.  
PA (RIEG) RIEGER D.  
PA (SHEN) SHENOY S.  
PA (SHIM) SHINKETS R.  
PA (SMIT) SMITHSON G.  
PA (STON) STONE D.  
PA (VERN) VERNET C.  
PA (VOSS) VOSS E.  
Query Match 5.9%; Score 70.5; DB 8; Length 343;  
Best Local Similarity 30.0%; Pred. No. 51;  
RESULT 1228  
ID ADY15182 standard; protein; 350 AA.  
DE PRO polypeptide SEQ ID NO 988.  
PN WO2005016962-A2.  
PD 24-FEB-2005  
PA (GETH) GENENTECH INC.  
Query Match 5.9%; Score 70.5; DB 9; Length 350;  
Best Local Similarity 18.5%; Pred. No. 52;  
RESULT 1229  
ID ADY15180 standard; protein; 350 AA.  
DE PRO polypeptide SEQ ID NO 986.  
PN WO2005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 5.9%; Score 70.5; DB 9; Length 350;  
Best Local Similarity 18.5%; Pred. No. 52;  
RESULT 1230  
ID ADR40543 standard; protein; 363 AA.  
DE Ovine melatonin receptor O4608 protein.  
PN US2004161823-A1.  
PD 19-AUG-2004.  
PA (FEDE) FEDER J N.  
PA (MINT) MINTIER G.  
PA (RAMA) RAMANATHAN C S.  
PA (HAWK) HAWKEN D R.  
Query Match 5.9%; Score 70.5; DB 8; Length 363;  
Best Local Similarity 23.1%; Pred. No. 55;  
RESULT 1231  
ID AAR65518 standard; protein; 365 AA.  
DE Prostaglandin-EP3-9 receptor.  
PN WO9500552-A1.  
PD 05-JAN-1995.  
PA (MERI) MERCK FROST CANADA INC.  
Query Match 5.9%; Score 70.5; DB 2; Length 365;  
Best Local Similarity 24.2%; Pred. No. 55;  
RESULT 1232  
ID AAE38521 standard; protein; 365 AA.  
DE Human PTGER3 protein isoform, EP3b.  
PN WO2003064471-A2.  
PD 07-AUG-2003.  
PA (DECO) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 365;  
Best Local Similarity 24.2%; Pred. No. 55;  
RESULT 1233  
ID ADI35077 standard; protein; 365 AA.  
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #9.  
PN US2003224393-A1.  
PD 04-DEC-2003.  
PA (DECO) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 8; Length 365;  
Best Local Similarity 24.2%; Pred. No. 55;  
RESULT 1234  
ID ADL15889 standard; protein; 365 AA.  
DE Human prostaglandin EP3 receptor #3.  
PN US6670134-B1.  
PD 30-DEC-2003.  
PA (ALLR) ALLERGAN INC.  
PA (UYAR) UNIV ARIZONA.  
Query Match 5.9%; Score 70.5; DB 8; Length 365;  
Best Local Similarity 24.2%; Pred. No. 55;  
RESULT 1235  
ID ADR67864 standard; protein; 365 AA.  
DE Prostaglandin E2 EP3 III.  
PN WO2004074830-A2.  
PD 02-SEP-2004.  
PA (PARB) BAYER HEALTHCARE AG.  
Query Match 5.9%; Score 70.5; DB 8; Length 365;  
Best Local Similarity 24.2%; Pred. No. 55;  
RESULT 1236  
ID ADS21429 standard; protein; 366 AA.  
DE Bacterial polypeptide #10462.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOI) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SIAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 5.9%; Score 70.5; DB 8; Length 366;  
Best Local Similarity 21.2%; Pred. No. 56;  
RESULT 1237  
ID ADF04359 standard; protein; 367 AA.  
DE Bacterial polypeptide #471.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 70.5; DB 7; Length 367;  
Best Local Similarity 33.3%; Pred. No. 56;  
RESULT 1238  
ID AAE38520 standard; protein; 374 AA.  
DE Human PTGER3 protein isoform, EP3d.  
PN WO2003064471-A2.  
PD 07-AUG-2003.  
PA (DECO) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 374;  
Best Local Similarity 24.2%; Pred. No. 57;  
RESULT 1239  
ID ADI35075 standard; protein; 374 AA.  
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8.  
PN US2003224393-A1.  
PD 04-DEC-2003.  
PA (DECO) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 8; Length 374;  
Best Local Similarity 24.2%; Pred. No. 57;  
RESULT 1240  
ID AAR48711 standard; protein; 379 AA.  
DE G-protein coupled rat serotonin 2 receptor protein.  
PN WO9405695-A1.  
PD 17-MAR-1994.  
PA (UYNY) UNIV NEW YORK STATE.  
Query Match 5.9%; Score 70.5; DB 2; Length 379;

Best Local Similarity 22.9%; Pred. No. 58;  
RESULT 1241  
ID AAM02683 standard; peptide; 379 AA.  
DE G-protein coupled rat serotonin 2 receptor.  
PN US508384-A.  
PD 16-APR-1996.  
PA (UYNY ) UNIV NEW YORK STATE.  
Query Match 5.9%; Score 70.5; DB 2; Length 379;  
Best Local Similarity 22.9%; Pred. No. 58;  
RESULT 1242  
ID AAR69517 standard; protein; 388 AA.  
DE Prostaglandin-EP3-2i receptor.  
PN W09500552-A1.  
PD 05-JAN-1995.  
PA (MERI ) MERCK FROSST CANADA INC.  
Query Match 5.9%; Score 70.5; DB 2; Length 388;  
Best Local Similarity 24.2%; Pred. No. 60;  
RESULT 1243  
ID AAE38513 standard; protein; 388 AA.  
DE Human PTER3 protein isoform, EP3C.  
PN W02003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 388;  
Best Local Similarity 24.2%; Pred. No. 60;  
RESULT 1244  
ID ADI35061 standard; protein; 388 AA.  
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #1.  
PN US2003224393-A1.  
PD 04-DEC-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 8; Length 388;  
Best Local Similarity 24.2%; Pred. No. 60;  
RESULT 1245  
ID ADL15887 standard; protein; 388 AA.  
DE Human prostaglandin EP3 receptor #2.  
PN US6670134-B1.  
PD 30-DEC-2003.  
PA (ALLR ) ALLERGAN INC.  
PA (UYAR-) UNIV ARIZONA.  
Query Match 5.9%; Score 70.5; DB 8; Length 388;  
Best Local Similarity 24.2%; Pred. No. 60;  
RESULT 1246  
ID ADI3753 standard; protein; 388 AA.  
DE Human prostaglandin E2 EP3 II polypeptide.  
PN W02004075813-A2.  
PD 10-SEP-2004.  
PA (FARB ) BAYER HEALTHCARE AG.  
Query Match 5.9%; Score 70.5; DB 8; Length 388;  
Best Local Similarity 24.2%; Pred. No. 60;  
RESULT 1247  
ID AAR69516 standard; protein; 390 AA.  
DE Prostaglandin-EP3-alpha receptor.  
PN W09500552-A1.  
PD 05-JAN-1995.  
PA (MERI ) MERCK FROSST CANADA INC.  
Query Match 5.9%; Score 70.5; DB 2; Length 390;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1248  
ID AAE38516 standard; protein; 390 AA.  
DE Human PTER3 protein isoform, EP3a1.  
PN W02003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 390;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1249  
ID AAE38517 standard; protein; 390 AA.  
DE Human PTER3 protein isoform, EP3a2.  
PN W02003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 390;

Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1250  
ID ADI35067 standard; protein; 390 AA.  
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.  
PN US2003224393-A1.  
PD 04-DEC-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1251  
ID ADI35069 standard; protein; 390 AA.  
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.  
PN US2003224393-A1.  
PD 04-DEC-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1252  
ID ADL15898 standard; protein; 390 AA.  
DE Human prostaglandin EP3 receptor #4.  
PN US6670134-B1.  
PD 30-DEC-2003.  
PA (ALLR ) ALLERGAN INC.  
PA (UYAR-) UNIV ARIZONA.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1253  
ID ADL15885 standard; protein; 390 AA.  
DE Human prostaglandin EP3 receptor #1.  
PN US6670134-B1.  
PD 30-DEC-2003.  
PA (ALLR ) ALLERGAN INC.  
PA (UYAR-) UNIV ARIZONA.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1254  
ID ADR70434 standard; protein; 390 AA.  
DE Human prostaglandin E2 EP3 protein.  
PN W02004074842-A2.  
PD 02-SEP-2004.  
PA (FARB ) BAYER HEALTHCARE AG.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1255  
ID ADI57616 standard; protein; 390 AA.  
DE Prostaglandin E2 EP3 I.  
PN W02004075814-A2.  
PD 10-SEP-2004.  
PA (FARB ) BAYER HEALTHCARE AG.  
Query Match 5.9%; Score 70.5; DB 8; Length 390;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1256  
ID AAM57411 standard; protein; 393 AA.  
DE Human prostaglandin EP3-VI receptor.  
PN JP1013185-A.  
PD 06-MAY-1998.  
PA (ONOV ) ONO PHARM CO LTD.  
Query Match 5.9%; Score 70.5; DB 2; Length 393;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1257  
ID AAE38519 standard; protein; 393 AA.  
DE Human PTER3 protein isoform, EP3e.  
PN W02003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.9%; Score 70.5; DB 7; Length 393;  
Best Local Similarity 24.2%; Pred. No. 61;  
RESULT 1258  
ID AAE38523 standard; protein; 393 AA.  
DE Human PTER3 protein isoform, EP3-VI.  
PN W02003064471-A2.  
PD 07-AUG-2003.  
PA (DECO-) DECODE GENETICS EHF.

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Query Match          5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 61;
RESULT 1259
ID ADI35081 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match          5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 61;
RESULT 1260
ID ADI35073 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match          5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 61;
RESULT 1261
ID AAW57410 standard; protein; 402 AA.
DE Human EP3-V receptor.
PN JP10113185-A.
PD 06-MAY-1998.
PA (ONOI) ONO PHARM CO LTD.
Query Match          5.9%; Score 70.5; DB 2; Length 402;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1262
ID ABP81904 standard; protein; 402 AA.
DE Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match          5.9%; Score 70.5; DB 6; Length 402;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1263
ID AAE38522 standard; protein; 402 AA.
DE Human PTGER3 protein isoform, EP3-V.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match          5.9%; Score 70.5; DB 7; Length 402;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1264
ID ADI35079 standard; protein; 402 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match          5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1265
ID ADO55167 standard; protein; 402 AA.
DE Human #69 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAN-) VAN ANDEL INST.
Query Match          5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1266
ID ADO29620 standard; protein; 402 AA.
DE Human GPCR PTGER3, SEQ ID NO:722.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match          5.9%; Score 70.5; DB 8; Length 402;
Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1267
ID ADZ09834 standard; protein; 402 AA.
DE Human breast cancer marker DKFZ586M0723 protein.
PN EP152594-A2.
PD 13-APR-2005.
PA (FARB) BAYER HEALTHCARE AG.
Query Match          5.9%; Score 70.5; DB 9; Length 402;

Best Local Similarity 24.2%; Pred. No. 63;
RESULT 1268
ID AAE38514 standard; protein; 407 AA.
DE Human PTGER3 protein isoform, EP3g.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match          5.9%; Score 70.5; DB 7; Length 407;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1269
ID ADI35063 standard; protein; 407 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match          5.9%; Score 70.5; DB 8; Length 407;
Best Local Similarity 24.2%; Pred. No. 64;
RESULT 1270
ID AAE38518 standard; protein; 425 AA.
DE Human PTGER3 protein isoform, EP3f.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match          5.9%; Score 70.5; DB 7; Length 425;
Best Local Similarity 24.2%; Pred. No. 68;
RESULT 1271
ID ADI35071 standard; protein; 425 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #6.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match          5.9%; Score 70.5; DB 8; Length 425;
Best Local Similarity 24.2%; Pred. No. 68;
RESULT 1272
ID AAE38515 standard; protein; 433 AA.
DE Human PTGER3 protein isoform, EP3n.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match          5.9%; Score 70.5; DB 7; Length 433;
Best Local Similarity 24.2%; Pred. No. 70;
RESULT 1273
ID ADI35065 standard; protein; 433 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match          5.9%; Score 70.5; DB 8; Length 433;
Best Local Similarity 24.2%; Pred. No. 70;
RESULT 1274
ID AAW98431 standard; protein; 480 AA.
DE H. pylori GHP 446 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR-) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match          5.9%; Score 70.5; DB 2; Length 480;
Best Local Similarity 23.1%; Pred. No. 81;
RESULT 1275
ID ADY09805 standard; protein; 494 AA.
DE Plant full length insert polypeptide seqid 65620.
PN US2004034888-A1.
PD 19-FEB-2004.
PA (LIUD/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOV/) CAO Y.
Query Match          5.9%; Score 70.5; DB 8; Length 494;
Best Local Similarity 21.4%; Pred. No. 84;
RESULT 1276
ID ABP40525 standard; protein; 499 AA.
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DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 5; Length 499;  
RESULT 1277  
ID ADS06092 standard; protein; 499 AA.  
DE Staphylococcus epidermis polypeptide seqid 5387.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (POUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 499;  
RESULT 1278  
ID ABB08338 standard; protein; 521 AA.  
DE Protein encoded by Prokaryotic essential gene #16000.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 6; Length 521;  
RESULT 1279  
ID AAV97213 standard; protein; 539 AA.  
DE Wheat sugar transport protein encoded by wlk8.pk0001.a11.  
PN US6383776-B1.  
PD 07-MAY-2002.  
PA (DUPO-) DU PONT DE NEMOURS & CO E. I.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 5; Length 539;  
RESULT 1280  
ID ABB08338 standard; protein; 539 AA.  
DE Wheat sugar transport protein #4.  
PN US2002178468-A1.  
PD 28-NOV-2002.  
PA (ALLE/) ALLEN S. M.  
PA (HITZ/) HITZ W. D.  
PA (KINN/) KINNEY A. J.  
PA (TING/) TRINGEY S. V.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 6; Length 539;  
RESULT 1281  
ID ADG47930 standard; protein; 539 AA.  
DE Wheat Beta-vulgaris-like sugar transport protein #1.  
PN US2002199217-A1.  
PD 26-DEC-2002.  
PA (HELE/) HELENTJARIIS T. G.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 539;  
RESULT 1282  
ID ABB27418 standard; protein; 548 AA.  
DE Protein encoded by Prokaryotic essential gene #12945.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 6; Length 548;  
RESULT 1283  
ID ADN22789 standard; protein; 556 AA.  
DE Bacterial polypeptide #5442.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G. J.  
PA (SLAT/) SLATER S. C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B. S.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 556;  
RESULT 1284  
ID ADD46023 standard; protein; 599 AA.  
DE Rat Protein P23978, SEQ ID NO 11695.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO-) GEN HOSPITAL CORP.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 7; Length 599;  
RESULT 1285  
ID ABB02687 standard; protein; 599 AA.  
DE Rattus norvegicus neuronal GABA transporter (GAT-1).  
PN US2003143729-A1.  
PD 31-JUL-2003.  
PA (SYNA-) SYNAPTIC PHARM CORP.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 7; Length 599;  
RESULT 1286  
ID AAM78767 standard; protein; 600 AA.  
DE Human protein SEQ ID NO 1429.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 4; Length 600;  
RESULT 1287  
ID ADJ64315 standard; protein; 662 AA.  
DE Cartilage differentiation inhibiting protein, SEQ ID 10.  
PN WO2004013326-A1.  
PD 12-FEB-2004.  
PA (ASAH-) ASAH KASEI KK.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 662;  
RESULT 1288  
ID ABB92892 standard; protein; 700 AA.  
DE Herbicidally active polypeptide SEQ ID NO 2103.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 5; Length 700;  
RESULT 1289  
ID AAB56721 standard; protein; 717 AA.  
DE Human prostate cancer antigen protein sequence SEQ ID NO:1299.  
PN WO200055174-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C. A.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 3; Length 717;  
RESULT 1290  
ID ADG47941 standard; protein; 740 AA.  
DE Arabidopsis thaliana-like sugar transport protein #2.  
PN US2002199217-A1.  
PD 26-DEC-2002.  
PA (HELE/) HELENTJARIIS T. G.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 740;  
RESULT 1291  
ID AAG39555 standard; protein; 766 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48959.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 3; Length 766;  
RESULT 1292  
ID AAG39554 standard; protein; 815 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48958.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 5.9%; Score 70.5; DB 3; Length 815;  
RESULT 1293  
ID AAG39553 standard; protein; 927 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48957.  
PN EPI033405-A2.

PD 06-SEP-2000.  
Query Match 5.9%; Score 70.5; DB 3; Length 927;  
Best Local Similarity 21.3%; Pred. No. 2e+02;  
RESULT 1294  
ID ABP73754 standard; protein; 1026 AA.  
DE Candida albicans essential protein SEQ ID NO 7591.  
PN WO200253728-A2.  
PD 11-JUL-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 70.5; DB 5; Length 1026;  
Best Local Similarity 22.3%; Pred. No. 2.3e+02;  
RESULT 1295  
ID AAM17057 standard; protein; 1027 AA.  
DE Candida albicans chitin synthase (CHS1).  
PN WO9716540-A1.  
PD 09-MAY-1997.  
PA (CHEM-) CHEMGENICS PHARM INC.  
Query Match 5.9%; Score 70.5; DB 2; Length 1027;  
Best Local Similarity 22.3%; Pred. No. 2.3e+02;  
RESULT 1296  
ID ADH22510 standard; protein; 1147 AA.  
DE Human transporter & ion channel (TRICH) protein SeqID8.  
PN WO2003093444-A2.  
PD 13-NOV-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 5.9%; Score 70.5; DB 8; Length 1147;  
Best Local Similarity 19.5%; Pred. No. 2.7e+02;  
RESULT 1297  
ID ADK18350 standard; protein; 1163 AA.  
DE Human NOVX protein #2.  
PN WO2003057854-A2.  
PD 17-JUL-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.9%; Score 70.5; DB 7; Length 1163;  
Best Local Similarity 19.5%; Pred. No. 2.8e+02;  
RESULT 1298  
ID ADM29274 standard; protein; 1163 AA.  
DE Human novel protein NOV2b.  
PN WO2003064628-A2.  
PD 07-AUG-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.9%; Score 70.5; DB 7; Length 1163;  
Best Local Similarity 19.5%; Pred. No. 2.8e+02;  
RESULT 1299  
ID AAM53863 standard; peptide; 1780 AA.  
DE Human gravin polypeptide.  
PN US5741890-A.  
PD 21-APR-1998.  
PA (UYOR-) UNIV OREGON HEALTH SCI.  
Query Match 5.9%; Score 70.5; DB 2; Length 1780;  
Best Local Similarity 34.8%; Pred. No. 5e+02;  
RESULT 1300  
ID AAB15380 standard; protein; 1780 AA.  
DE Human gravin protein sequence.  
PN US6090929-A.  
PD 18-JUL-2000.  
PA (UYOR-) UNIV OREGON HEALTH SCI.  
Query Match 5.9%; Score 70.5; DB 3; Length 1780;  
Best Local Similarity 34.8%; Pred. No. 5e+02;  
RESULT 1301  
ID AAO17365 standard; protein; 1781 AA.  
DE Human gravin.  
PN EP19107-A2.  
PD 27-MAR-2002.  
PA (SCHD-) SCHERING AG.  
Query Match 5.9%; Score 70.5; DB 5; Length 1781;  
Best Local Similarity 34.8%; Pred. No. 5e+02;  
RESULT 1302  
ID ABU03477 standard; protein; 1781 AA.  
DE Angiogenesis-associated human protein sequence #22.  
PN WO200279492-A2.  
PD 10-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match 5.9%; Score 70.5; DB 6; Length 1781;  
Best Local Similarity 34.8%; Pred. No. 5e+02;  
RESULT 1303  
ID ABB97448 standard; protein; 1783 AA.  
DE Novel human protein SEQ ID NO: 716.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.9%; Score 70.5; DB 5; Length 1783;  
Best Local Similarity 34.8%; Pred. No. 5e+02;  
RESULT 1304  
ID ABG21018 standard; protein; 1795 AA.  
DE Novel human diagnostic protein #21009.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.9%; Score 70.5; DB 4; Length 1795;  
Best Local Similarity 34.8%; Pred. No. 5e+02;  
RESULT 1305  
ID AAG34242 standard; protein; 185 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41631.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.9%; Score 70.5; DB 3; Length 185;  
Best Local Similarity 26.2%; Pred. No. 25;  
RESULT 1306  
ID AAG34241 standard; protein; 189 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41630.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.9%; Score 70.5; DB 3; Length 189;  
Best Local Similarity 26.2%; Pred. No. 25;  
RESULT 1307  
ID AAM44944 standard; protein; 225 AA.  
DE Avian infectious bronchitis virus glycoprotein M.  
PN FR2751225-A1.  
PD 23-JAN-1998.  
PA (INMR-) RHONE MERIEUX SA.  
Query Match 5.9%; Score 70.5; DB 2; Length 225;  
Best Local Similarity 21.6%; Pred. No. 32;  
RESULT 1308  
ID ADB09893 standard; protein; 226 AA.  
DE Alloiococcus oclitis antigenic protein SEQ ID NO:3730.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP-) WYETH HOLDINGS CORP.  
Query Match 5.9%; Score 70.5; DB 6; Length 226;  
Best Local Similarity 24.1%; Pred. No. 33;  
RESULT 1309  
ID AAG34240 standard; protein; 235 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 41629.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.9%; Score 70.5; DB 3; Length 235;  
Best Local Similarity 26.2%; Pred. No. 34;  
RESULT 1310  
ID ABB69790 standard; protein; 256 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 36162.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 5.9%; Score 70.5; DB 4; Length 256;  
Best Local Similarity 20.2%; Pred. No. 39;  
RESULT 1311  
ID ADS96502 standard; protein; 256 AA.  
DE Drosophila melanogaster protein, SEQ ID 123.  
PN WO2004039999-A2.  
PD 13-MAY-2004.  
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.9%; Score 70.5; DB 8; Length 256;  
Best Local Similarity 20.2%; Pred. No. 39;  
RESULT 1312  
ID ADT05703 standard; protein; 256 AA.

DE Haemophilus influenzae (NTHI) protein - SEQ ID 739.  
PN WO2004078949-A2.  
PA (CHIL-) CHILDRENS HOSPITAL INC.  
Query Match 5.9%; Score 70; DB 8; Length 256;  
Best Local Similarity 18.3%; Pred. No. 39;  
RESULT 1313  
ID AAG53762 standard; protein; 274 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68478.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.9%; Score 70; DB 3; Length 274;  
Best Local Similarity 26.0%; Pred. No. 43;  
RESULT 1314  
ID AAG53761 standard; protein; 287 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68477.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 5.9%; Score 70; DB 3; Length 287;  
Best Local Similarity 26.0%; Pred. No. 45;  
RESULT 1315  
ID ABU35677 standard; protein; 292 AA.  
DE Protein encoded by Prokaryotic essential gene #21204.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 70; DB 6; Length 292;  
Best Local Similarity 22.5%; Pred. No. 47;  
RESULT 1316  
ID ADK48488 standard; protein; 307 AA.  
DE Streptococcus pneumoniae protein, Seq ID No 5003.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 70; DB 8; Length 307;  
Best Local Similarity 26.2%; Pred. No. 50;  
RESULT 1317  
ID AAR72985 standard; protein; 333 AA.  
DE Epsilon opioid receptor.  
PN WO9512670-A1.  
PD 11-MAY-1995.  
PA (ALCO-) ALCOHOLISM & DRUG ADDICTION RES FOUND.  
Query Match 5.9%; Score 70; DB 2; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1318  
ID AAY90613 standard; protein; 333 AA.  
DE Human G protein-coupled receptor GPR8.  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 70; DB 3; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1319  
ID AAY90647 standard; protein; 333 AA.  
DE Human mutant G protein-coupled receptor GPR8 (T259K).  
PN WO200022129-A1.  
PD 20-APR-2000.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 70; DB 3; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1320  
ID AAU01297 standard; protein; 333 AA.  
DE Human G-protein receptor 8, GPR 8, mutant N127A.  
PN WO200127632-A2.  
PD 19-APR-2001.  
PA (CAMP-) CAMBRIDGE DRUG DISCOVERY LTD.  
PA (WILL/) WILLIAMS K M.  
Query Match 5.9%; Score 70; DB 4; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1321  
ID AAU01295 standard; protein; 333 AA.  
DE Human G-protein receptor 8, GPR 8.  
PN WO200127632-A2.

PD 19-APR-2001.  
PA (CAMP-) CAMBRIDGE DRUG DISCOVERY LTD.  
PA (WILL/) WILLIAMS K M.  
Query Match 5.9%; Score 70; DB 4; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1322  
ID AAU01298 standard; protein; 333 AA.  
DE Human G-protein receptor 8, GPR 8, mutant T259E.  
PN WO200127632-A2.  
PD 19-APR-2001.  
PA (CAMP-) CAMBRIDGE DRUG DISCOVERY LTD.  
PA (WILL/) WILLIAMS K M.  
Query Match 5.9%; Score 70; DB 4; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1323  
ID ABB84683 standard; protein; 333 AA.  
DE Human GPR8-ligand related protein #1.  
PN WO200198494-A1.  
PD 27-DEC-2001.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 5; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1324  
ID ABB84723 standard; protein; 333 AA.  
DE Human GPR8-ligand related protein #3.  
PN WO200198494-A1.  
PD 27-DEC-2001.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 5; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1325  
ID ABG65918 standard; protein; 333 AA.  
DE G protein-coupled receptor related peptide #6.  
PN WO200244368-A1.  
PD 06-JUN-2002.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 5; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1326  
ID ABU61448 standard; protein; 333 AA.  
DE Screening method related protein #1.  
PN WO200293161-A1.  
PD 21-NOV-2002.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 6; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1327  
ID ABJ37874 standard; protein; 333 AA.  
DE GPR7 ligand related human protein SEQ ID No 84.  
PN WO2002102847-A1.  
PD 27-DEC-2002.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 6; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1328  
ID ABR81897 standard; protein; 333 AA.  
DE Human G protein-coupled receptor GPR8 protein SEQ ID NO:279.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 5.9%; Score 70; DB 6; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1329  
ID ABR57245 standard; protein; 333 AA.  
DE Human GPR8 protein SEQ ID NO:84.  
PN WO2003045994-A1.  
PD 05-JUN-2003.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1330  
ID ADC22691 standard; protein; 333 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #44.

PN US655339-B1.  
ID 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1331  
ID ADG22535 standard; protein; 333 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #5.  
PN US655339-B1.  
PD 29-APR-2003.  
PA (AREN-) ARENA PHARM INC.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1332  
ID ADG51793 standard; protein; 333 AA.  
DE Human GPR8, SEQ ID 4.  
PN WO2003057236-A1.  
PD 17-JUL-2003.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1333  
ID ABR61545 standard; protein; 333 AA.  
DE Human GPR8 receptor polypeptide.  
PN WO2003081234-A2.  
PD 02-OCT-2003.  
PA (FARB-) BAYER AG.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1334  
ID ADG41976 standard; protein; 333 AA.  
DE Human GPR8 polypeptide.  
PN JP2003009867-A.  
PD 14-JUN-2003.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1335  
ID ADH14008 standard; protein; 333 AA.  
DE Human GPR8.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAM/) LIAM C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1336  
ID ADH14164 standard; protein; 333 AA.  
DE Mutated human GPR8.  
PN US2003105292-A1.  
PD 05-JUN-2003.  
PA (LIAM/) LIAM C W.  
PA (BEHA/) BEHAN D P.  
PA (CHAL/) CHALMERS D T.  
Query Match 5.9%; Score 70; DB 7; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1337  
ID ADG12852 standard; protein; 333 AA.  
DE Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.  
PN WO2003097795-A2.  
PD 27-NOV-2003.  
PA (NORA-) NORAK BIOSCI INC.  
Query Match 5.9%; Score 70; DB 8; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1338  
ID ADO29700 standard; protein; 333 AA.  
DE Human GPCR GPR8, SEQ ID NO:802.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 5.9%; Score 70; DB 8; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;

RESULT 1339  
ID ADO31044 standard; protein; 333 AA.  
DE Human GPR8 protein SEQ ID NO:73.  
PN WO2004041301-A1.  
PD 21-MAY-2004.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 8; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1340  
ID ADQ19919 standard; protein; 333 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.9%; Score 70; DB 8; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1341  
ID ADS14162 standard; protein; 333 AA.  
DE Human GPR8 ligand protein SeqID 73.  
PN WO2004080485-A1.  
PD 23-SEP-2004.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 5.9%; Score 70; DB 8; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1342  
ID ADV24041 standard; protein; 333 AA.  
DE Neuropeptide w antibody associated polypeptide seqid 17.  
PN WO2004106382-A1.  
PD 09-DEC-2004.  
PA (TAKE-) TAKEDA PHARM CO LTD.  
Query Match 5.9%; Score 70; DB 9; Length 333;  
Best Local Similarity 23.6%; Pred. No. 56;  
RESULT 1343  
ID ADG12854 standard; protein; 347 AA.  
DE Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.  
PN WO2003097795-A2.  
PD 27-NOV-2003.  
PA (NORA-) NORAK BIOSCI INC.  
Query Match 5.9%; Score 70; DB 8; Length 347;  
Best Local Similarity 23.6%; Pred. No. 59;  
RESULT 1344  
ID ABR30839 standard; protein; 364 AA.  
DE Human calcium channel protein.  
PN WO200252003-A2.  
PD 04-JUL-2002.  
PA (FARB-) BAYER AG.  
Query Match 5.9%; Score 70; DB 5; Length 364;  
Best Local Similarity 25.0%; Pred. No. 63;  
RESULT 1345  
ID ADG12856 standard; protein; 364 AA.  
DE Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.  
PN WO2003097795-A2.  
PD 27-NOV-2003.  
PA (NORA-) NORAK BIOSCI INC.  
Query Match 5.9%; Score 70; DB 8; Length 364;  
Best Local Similarity 23.6%; Pred. No. 63;  
RESULT 1346  
ID ADO28778 standard; protein; 364 AA.  
DE Human GPR8-enhanced receptor.  
PN US2004091946-A1.  
PD 13-MAY-2004.  
PA (OAKL/) OAKLEY R H.  
PA (BARA/) BARAK L S.  
PA (LAPO/) LAPORTE S A.  
PA (CARO/) CARON M G.  
Query Match 5.9%; Score 70; DB 8; Length 364;  
Best Local Similarity 23.6%; Pred. No. 63;  
RESULT 1347  
ID ADX44597 standard; protein; 364 AA.  
DE Enhanced human G-protein coupled receptor 8 - SEQ ID 56.  
PN WO2005012876-A2.  
PD 10-FEB-2005.  
PA (NORA-) NORAK BIOSCIENCES INC.



Query Match 5.9%; Score 70; DB 9; Length 364;  
Best Local Similarity 23.6%; Pred. No. 63;  
RESULT 1348  
ID ADY83827 standard; protein; 364 AA.  
DE hGPR8-enhanced receptor.  
PN WO2005029035-A2.  
PD 31-MAR-2005.  
PA (NORA-) NORAK BIOSCIENCES INC.  
Query Match 5.9%; Score 70; DB 9; Length 364;  
Best Local Similarity 23.6%; Pred. No. 63;  
RESULT 1349  
ID ADG12858 standard; protein; 378 AA.  
DE HA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.  
PN WO2003097795-A2.  
PD 27-NOV-2003.  
PA (NORA-) NORAK BIOSCI INC.  
Query Match 5.9%; Score 70; DB 8; Length 378;  
Best Local Similarity 23.6%; Pred. No. 67;  
RESULT 1350  
ID ADN49121 standard; protein; 388 AA.  
DE Mouse oxytocin receptor protein.  
PN US2004086881-A1.  
PD 06-MAY-2004.  
PA (PAMA/) RAMANATHAN C S.  
PA (GOPA/) GOPAL S.  
PA (MINT/) MINTIER G A.  
PA (FEDE/) FEDER J.  
Query Match 5.9%; Score 70; DB 8; Length 388;  
Best Local Similarity 24.8%; Pred. No. 69;  
RESULT 1351  
ID ADO29591 standard; protein; 388 AA.  
DE Mouse GPCR OXTR, SEQ ID NO:693.  
PN WO2004040000-A2.  
PD 13-MAY-2004.  
PA (PRIM-) PRIMAL INC.  
Query Match 5.9%; Score 70; DB 8; Length 388;  
Best Local Similarity 24.8%; Pred. No. 69;  
RESULT 1352  
ID ADA54410 standard; protein; 399 AA.  
DE Human protein, SEQ ID 1978.  
PN EPI293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.9%; Score 70; DB 6; Length 399;  
Best Local Similarity 22.9%; Pred. No. 72;  
RESULT 1353  
ID ABG99947 standard; protein; 399 AA.  
DE Human novel polypeptide #60.  
PN WO200274961-A1.  
PD 26-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.9%; Score 70; DB 6; Length 399;  
Best Local Similarity 22.9%; Pred. No. 72;  
RESULT 1354  
ID ADC96947 standard; protein; 425 AA.  
DE E. faecium protein sequence SEQ ID 6574.  
PN US6583375-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 70; DB 7; Length 425;  
Best Local Similarity 25.9%; Pred. No. 78;  
RESULT 1355  
ID ADA34110 standard; protein; 470 AA.  
DE Acinetobacter baumannii protein #1271.  
PN US662958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 70; DB 6; Length 470;  
Best Local Similarity 23.5%; Pred. No. 90;  
ID ABM67264 standard; protein; 474 AA.  
DE Photorhabdus luminescens protein sequence #361.

PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70; DB 6; Length 474;  
Best Local Similarity 22.9%; Pred. No. 91;  
RESULT 1357  
ID AAE16787 standard; protein; 475 AA.  
DE Human transporter and ion channel-24 (TRICH-24) protein.  
PN WO200192304-A2.  
PD 06-DEC-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.9%; Score 70; DB 5; Length 475;  
Best Local Similarity 25.0%; Pred. No. 91;  
RESULT 1358  
ID ADA89683 standard; protein; 506 AA.  
DE Staphylococcus aureus antigenic protein #222.  
PN WO2003011899-A2.  
PD 13-FEB-2003.  
PA (UTSH-) UNIV SHEPFIELD.  
PA (BIOS-) BIOSINEXUS INC.  
Query Match 5.9%; Score 70; DB 6; Length 506;  
Best Local Similarity 20.1%; Pred. No. 1e+02;  
RESULT 1359  
ID ABM72414 standard; protein; 506 AA.  
DE Staphylococcus aureus protein #1654.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 5.9%; Score 70; DB 6; Length 506;  
Best Local Similarity 20.1%; Pred. No. 1e+02;  
RESULT 1360  
ID AAE21176 standard; protein; 540 AA.  
DE Human TRICH-20 protein.  
PN WO200212340-A2.  
PD 14-FEB-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.9%; Score 70; DB 5; Length 540;  
Best Local Similarity 25.0%; Pred. No. 1.1e+02;  
RESULT 1361  
ID AAM39017 standard; protein; 552 AA.  
DE Human polypeptide SEQ ID NO 2162.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.9%; Score 70; DB 4; Length 552;  
Best Local Similarity 25.0%; Pred. No. 1.1e+02;  
RESULT 1362  
ID ABU18262 standard; protein; 602 AA.  
DE Protein encoded by Prokaryotic essential gene #3789.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 70; DB 6; Length 602;  
Best Local Similarity 26.4%; Pred. No. 1.3e+02;  
RESULT 1363  
ID ABU33453 standard; protein; 637 AA.  
DE Protein encoded by Prokaryotic essential gene #18980.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.9%; Score 70; DB 6; Length 637;  
Best Local Similarity 23.1%; Pred. No. 1.4e+02;  
RESULT 1364  
ID AEB39900 standard; protein; 637 AA.  
DE L. pneumophila protein SEQ ID NO 4232.  
PN WO2005049642-A2.  
PD 02-JUN-2005.  
PA (INSP) INST PASTEUR.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UPLY-) UNIV LYON 1 BERNARD CLAUDE.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70; DB 9; Length 637;

Best Local Similarity 22.3%; Pred. No. 1.4e+02;  
RESULT 1365  
ID AAY91335 standard; protein; 640 AA.  
DE Group B Streptococcus protein sequence SEQ ID NO:68.  
PN W0200006736-A2.  
PD 10-FEB-2000.  
PA (MICR-) MICROBIAL TECHNIQS LTD.  
Query Match 5.9%; Score 70; DB 3; Length 640;  
Best Local Similarity 21.4%; Pred. No. 1.4e+02;  
RESULT 1366  
ID AEB36499 standard; protein; 647 AA.  
DE I. pneumoniae protein seq ID NO 831.  
PN W02005049642-A2.  
PD 02-JUN-2005.  
PA (INSP) INST PASTEUR.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
PA (UPLY-) UNIV LYON I BERNARD CLAUDE.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70; DB 9; Length 647;  
Best Local Similarity 22.3%; Pred. No. 1.4e+02;  
RESULT 1367  
ID AAM83819 standard; protein; 695 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4067.  
PN W02004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 5.9%; Score 70; DB 8; Length 695;  
Best Local Similarity 28.6%; Pred. No. 1.5e+02;  
RESULT 1368  
ID ADL04660 standard; protein; 767 AA.  
DE M. catarrhalis protein #426.  
PN US6673910-B1.  
PD 06-JAN-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.9%; Score 70; DB 8; Length 767;  
Best Local Similarity 21.3%; Pred. No. 1.8e+02;  
RESULT 1369  
ID AAR53921 standard; protein; 980 AA.  
DE HCV fusion protein corresp. to N-terminal of ORF.  
PN JP06092996-A.  
PD 05-APR-1994.  
PA (SHIM/) SHIMOTOYA K.  
Query Match 5.9%; Score 70; DB 2; Length 980;  
Best Local Similarity 24.6%; Pred. No. 2.5e+02;  
RESULT 1370  
ID ADS24062 standard; protein; 1041 AA.  
DE Bacterial polypeptide #13095.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.9%; Score 70; DB 8; Length 1041;  
Best Local Similarity 23.4%; Pred. No. 2.7e+02;  
RESULT 1371  
ID ADU69762 standard; protein; 1049 AA.  
DE S agalactiae hyperimmune serum reactive antigen seqid 457.  
PN W0200409242-A2.  
PD 18-NOV-2004.  
PA (INTE-) INTERCELL AG.  
Query Match 5.9%; Score 70; DB 8; Length 1049;  
Best Local Similarity 18.8%; Pred. No. 2.7e+02;  
RESULT 1372  
ID ADU69581 standard; protein; 1049 AA.  
DE S agalactiae hyperimmune serum reactive antigen seqid 276.  
PN W0200409242-A2.  
PD 18-NOV-2004.  
PA (INTE-) INTERCELL AG.  
Query Match 5.9%; Score 70; DB 8; Length 1049;  
Best Local Similarity 18.8%; Pred. No. 2.7e+02;  
RESULT 1373  
ID ADU69756 standard; protein; 1049 AA.  
DE S agalactiae hyperimmune serum reactive antigen seqid 451.  
PN W0200409242-A2.  
PD 18-NOV-2004.  
PA (INTE-) INTERCELL AG.  
Query Match 5.9%; Score 70; DB 8; Length 1049;  
Best Local Similarity 18.8%; Pred. No. 2.7e+02;  
RESULT 1374  
ID ADV87847 standard; protein; 1049 AA.  
DE Streptococcus agalactiae protein sequence, SEQ ID 241.  
PN FR2824074-A1.  
PD 31-OCT-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70; DB 8; Length 1049;  
Best Local Similarity 18.8%; Pred. No. 2.7e+02;  
RESULT 1375  
ID ADV79100 standard; protein; 1049 AA.  
DE Streptococcus agalactiae protein, SEQ ID 241.  
PN W0200292818-A2.  
PD 21-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70; DB 8; Length 1049;  
Best Local Similarity 18.8%; Pred. No. 2.7e+02;  
RESULT 1376  
ID ADV82666 standard; protein; 1049 AA.  
DE Streptococcus agalactiae protein, SEQ ID 3807.  
PN W0200292818-A2.  
PD 21-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70; DB 8; Length 1049;  
Best Local Similarity 18.8%; Pred. No. 2.7e+02;  
RESULT 1377  
ID ADV81299 standard; protein; 1049 AA.  
DE Streptococcus agalactiae protein, SEQ ID 2440.  
PN W0200292818-A2.  
PD 21-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70; DB 8; Length 1049;  
Best Local Similarity 18.8%; Pred. No. 2.7e+02;  
RESULT 1378  
ID ADV82607 standard; protein; 1049 AA.  
DE Streptococcus agalactiae protein, SEQ ID 3748.  
PN W0200292818-A2.  
PD 21-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.9%; Score 70; DB 8; Length 1049;  
Best Local Similarity 18.8%; Pred. No. 2.7e+02;  
RESULT 1379  
ID ADP07803 standard; protein; 138 AA.  
DE Human secreted protein, seq id 286.  
PN W02004042000-A2.  
PD 21-MAY-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.8%; Score 69.5; DB 8; Length 138;  
Best Local Similarity 22.0%; Pred. No. 19;  
RESULT 1380  
ID ADA33664 standard; protein; 198 AA.  
DE Acinetobacter baumannii protein #825.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 6; Length 198;  
Best Local Similarity 23.3%; Pred. No. 31;  
RESULT 1381  
ID ADB09276 standard; protein; 201 AA.  
DE Alloiococcus otitis antigenic protein SEQ ID NO:3216.  
PN W02003048304-A2.  
PD 12-JUN-2003.

PA (AMHP) WYETH HOLDINGS CORP.  
 Query Match 5.8%; Score 69.5; DB 6; Length 201;  
 Best Local Similarity 26.0%; Pred. No. 32;  
 RESULT 1382  
 ID AEB41646 standard; protein; 201 AA.  
 DE L. pneumophila protein SEQ ID NO 5978.  
 PN W02005048642-A2.  
 PD 02-JUN-2005.  
 PA (INSP) INST PASTEUR.  
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA (UYLY) UNIV LYON 1 BERNARD CLAUDE.  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 Query Match 5.8%; Score 69.5; DB 9; Length 201;  
 Best Local Similarity 17.6%; Pred. No. 32;  
 RESULT 1383  
 ID AAU29449 standard; protein; 210 AA.  
 DE Human G protein-coupled receptor (GPCR) polypeptide #70.  
 PN W0200168858-A2.  
 PD 20-SEP-2001.  
 PA (PHAA) PHARMACIA & UPJOHN CO.  
 Query Match 5.8%; Score 69.5; DB 4; Length 210;  
 Best Local Similarity 20.9%; Pred. No. 34;  
 RESULT 1384  
 ID ABG60737 standard; protein; 210 AA.  
 DE Novel G protein coupled receptor (nGPR-x) #70.  
 PN US2002058306-A1.  
 PD 16-MAY-2002.  
 PA (VOGE/) VOGELI G.  
 Query Match 5.8%; Score 69.5; DB 5; Length 210;  
 Best Local Similarity 20.9%; Pred. No. 34;  
 RESULT 1385  
 ID AAU01288 standard; protein; 218 AA.  
 DE Brassica napus fatty acid desaturase, Fad3C, mutant partial sequence.  
 PN W0200125453-A2.  
 PD 12-APR-2001.  
 PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
 Query Match 5.8%; Score 69.5; DB 4; Length 218;  
 Best Local Similarity 29.3%; Pred. No. 36;  
 RESULT 1386  
 ID ADB09278 standard; protein; 247 AA.  
 DE Allostercoccus otilis antigenic protein SEQ ID NO:3218.  
 PN W02002046304-A2.  
 PD 12-JUN-2003.  
 PA (AMHP) WYETH HOLDINGS CORP.  
 Query Match 5.8%; Score 69.5; DB 6; Length 247;  
 Best Local Similarity 26.0%; Pred. No. 42;  
 RESULT 1387  
 ID ABG66935 standard; protein; 253 AA.  
 DE Novel G-protein coupled receptor related protein #12.  
 PN W0200240539-A2.  
 PD 23-MAY-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 5.8%; Score 69.5; DB 5; Length 253;  
 Best Local Similarity 24.2%; Pred. No. 44;  
 RESULT 1388  
 ID ABG62542 standard; protein; 261 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 14418.  
 PN W0200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 5.8%; Score 69.5; DB 4; Length 261;  
 Best Local Similarity 27.7%; Pred. No. 46;  
 RESULT 1389  
 ID ABO80446 standard; protein; 270 AA.  
 DE Pseudomonas aeruginosa polypeptide #12621.  
 PN US551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.8%; Score 69.5; DB 7; Length 270;  
 Best Local Similarity 22.1%; Pred. No. 48;  
 RESULT 1390  
 ID ADB66076 standard; protein; 296 AA.  
 DE Streptomyces hygroscopicus ABC transporter.

PN W02003082909-A1.  
 PD 09-OCT-2003.  
 PA (AMHP) WYETH.  
 Query Match 5.8%; Score 69.5; DB 7; Length 296;  
 Best Local Similarity 21.0%; Pred. No. 54;  
 RESULT 1391  
 ID AAG71524 standard; protein; 308 AA.  
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1205.  
 PN W0200127158-A2.  
 PD 19-APR-2001.  
 PA (DIGI-) DIGISCENTS.  
 PA (YEDA) YEDA RES & DEV CO LTD.  
 Query Match 5.8%; Score 69.5; DB 4; Length 308;  
 Best Local Similarity 20.9%; Pred. No. 57;  
 RESULT 1392  
 ID ABB44525 standard; protein; 308 AA.  
 DE Human GPCR3 polypeptide SEQ ID NO 9.  
 PN W0200174904-A2.  
 PD 11-OCT-2001.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 5.8%; Score 69.5; DB 4; Length 308;  
 Best Local Similarity 20.9%; Pred. No. 57;  
 RESULT 1393  
 ID AAU24742 standard; protein; 308 AA.  
 DE Human olfactory receptor AOLF242.  
 PN W0200168805-A2.  
 PD 20-SEP-2001.  
 PA (SENO-) SENOMYX INC.  
 Query Match 5.8%; Score 69.5; DB 4; Length 308;  
 Best Local Similarity 20.9%; Pred. No. 57;  
 RESULT 1394  
 ID ABB95703 standard; protein; 308 AA.  
 DE Human GPCR polypeptide SEQ ID NO 216.  
 PN W0200216548-A2.  
 PD 28-FEB-2002.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Query Match 5.8%; Score 69.5; DB 5; Length 308;  
 Best Local Similarity 20.9%; Pred. No. 57;  
 RESULT 1395  
 ID AAU95729 standard; protein; 308 AA.  
 DE Human olfactory and pheromone G protein-coupled receptor #216.  
 PN W0200224726-A2.  
 PD 28-MAR-2002.  
 PA (CHEM-) CHEMCOM SA.  
 Query Match 5.8%; Score 69.5; DB 5; Length 308;  
 Best Local Similarity 20.9%; Pred. No. 57;  
 RESULT 1396  
 ID AAU85362 standard; protein; 308 AA.  
 DE G-coupled olfactory receptor #223.  
 PN W0200198526-A2.  
 PD 27-DEC-2001.  
 PA (SENO-) SENOMYX INC.  
 Query Match 5.8%; Score 69.5; DB 5; Length 308;  
 Best Local Similarity 20.9%; Pred. No. 57;  
 RESULT 1397  
 ID ADC86333 standard; protein; 308 AA.  
 DE Human GPCR protein SEQ ID NO:786.  
 PN EP1270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 Query Match 5.8%; Score 69.5; DB 7; Length 308;  
 Best Local Similarity 20.9%; Pred. No. 57;  
 RESULT 1398  
 ID ABW02126 standard; protein; 308 AA.  
 DE Human GPCR3 protein.  
 PN US2003195335-A1.  
 PD 16-OCT-2003.  
 PA (GROS/) GROSSE W M.  
 PA (SZER/) SZEKERES E S.  
 PA (CASW/) CASMAN S.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (BURG/) BURGESS C E.

PA (PADI/) PADIGARU M.  
PA (TAYL/) TAYLOR S.  
PA (TCHER/) TCHERNEV V T.  
PA (SPYR/) SPYTEK K A.  
PA (LITL/) LI L.  
PA (SHEN/) SHENOV S.  
PA (KEKU/) KEKUDA R.  
PA (GANG/) GANGOLLI E A.  
PA (STON/) STONE D J.  
PA (SMIT/) SMITHSON G.  
PA (MACO/) MACDOUGALL J R.  
Query Match 5.8%; Score 69.5; DB 7; Length 308;  
Best Local Similarity 20.9%; Pred. No. 57;  
RESULT 1399  
ID ABR01671 standard; protein; 316 AA.  
DE Human G protein coupled receptor SEQ ID 202.  
PN W02003000735-A2.  
PD 03-JAN-2003.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 5.8%; Score 69.5; DB 6; Length 316;  
Best Local Similarity 20.9%; Pred. No. 59;  
RESULT 1400  
ID ADU20551 standard; protein; 317 AA.  
DE A. thaliana At5g67210 homologue.  
PN W02004092349-A2.  
PD 28-OCT-2004.  
PA (BADI-) BASF PLANT SCI GMBH.  
Query Match 5.8%; Score 69.5; DB 8; Length 317;  
Best Local Similarity 33.7%; Pred. No. 60;  
RESULT 1401  
ID ADU20398 standard; protein; 317 AA.  
DE A. thaliana drought tolerance-associated protein At5g67210.  
PN W02004092349-A2.  
PD 28-OCT-2004.  
PA (BADI-) BASF PLANT SCI GMBH.  
Query Match 5.8%; Score 69.5; DB 8; Length 317;  
Best Local Similarity 33.7%; Pred. No. 60;  
RESULT 1402  
ID AAY35360 standard; protein; 321 AA.  
DE Chlamydia pneumoniae involved in the virulence process.  
PN W09927105-A2.  
PD 03-JUN-1999.  
PA (GENE-) GENSET.  
Query Match 5.8%; Score 69.5; DB 2; Length 321;  
Best Local Similarity 21.4%; Pred. No. 61;  
RESULT 1403  
ID ADC33485 standard; protein; 321 AA.  
DE Yeast ARV1.  
PN US6566512-B1.  
PD 20-MAY-2003.  
PA (UYCO-) UNIV COLUMBIA NEW YORK.  
Query Match 5.8%; Score 69.5; DB 7; Length 321;  
Best Local Similarity 18.8%; Pred. No. 61;  
RESULT 1404  
ID ADE37749 standard; protein; 321 AA.  
DE Yeast ARV1 (AR8-2 Required for viability).  
PN US2003186879-A1.  
PD 02-OCT-2003.  
PA (UYCO-) UNIV COLUMBIA NEW YORK.  
Query Match 5.8%; Score 69.5; DB 7; Length 321;  
Best Local Similarity 18.8%; Pred. No. 61;  
RESULT 1405  
ID AAY53139 standard; protein; 327 AA.  
DE Propionibacterium acnes immunogenic protein #14035.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 5.8%; Score 69.5; DB 4; Length 327;  
Best Local Similarity 25.5%; Pred. No. 62;  
RESULT 1406  
ID ABM49568 standard; protein; 327 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14334.  
PN W02003033515-A1.

PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.8%; Score 69.5; DB 6; Length 327;  
Best Local Similarity 25.5%; Pred. No. 62;  
RESULT 1407  
ID ADH10684 standard; protein; 354 AA.  
DE Rat Sprague-Dawley putative GCR polypeptide.  
PN W02003104484-A1.  
PD 18-DEC-2003.  
PA (META-) METABOLEX INC.  
Query Match 5.8%; Score 69.5; DB 8; Length 354;  
Best Local Similarity 22.0%; Pred. No. 70;  
RESULT 1408  
ID AAY05489 standard; protein; 382 AA.  
DE Human EDG-2 protein sequence.  
PN W09919513-A2.  
PD 22-APR-1999.  
PA (LXRB-) LXN BIOTECHNOLOGY INC.  
Query Match 5.8%; Score 69.5; DB 2; Length 382;  
Best Local Similarity 20.2%; Pred. No. 77;  
RESULT 1409  
ID AAU00302 standard; protein; 382 AA.  
DE LPA receptor-related amino acid sequence #1.  
PN W0200112838-A2.  
PD 22-FEB-2001.  
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.  
Query Match 5.8%; Score 69.5; DB 4; Length 382;  
Best Local Similarity 20.2%; Pred. No. 77;  
RESULT 1410  
ID ABG76099 standard; protein; 382 AA.  
DE Human lysophosphatidic acid (LPA) receptor EDG-1.  
PN US6485922-B1.  
PD 25-NOV-2002.  
PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 382;  
Best Local Similarity 20.2%; Pred. No. 77;  
RESULT 1411  
ID ABB47613 standard; protein; 400 AA.  
DE Listeria monocytogenes protein #317.  
PN W0200177335-A2.  
PD 18-OCT-2001.  
PA (INSP-) INST PASTEUR.  
Query Match 5.8%; Score 69.5; DB 5; Length 400;  
Best Local Similarity 22.9%; Pred. No. 82;  
RESULT 1412  
ID ABU32698 standard; protein; 400 AA.  
DE Protein encoded by Prokaryotic essential gene #18225.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 400;  
Best Local Similarity 22.9%; Pred. No. 82;  
RESULT 1413  
ID ADL12060 standard; protein; 401 AA.  
DE Drosophila dmtip1 protein.  
PN W02003002137-A2.  
PD 09-JAN-2003.  
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
Query Match 5.8%; Score 69.5; DB 7; Length 401;  
Best Local Similarity 20.9%; Pred. No. 83;  
RESULT 1414  
ID ABB60948 standard; protein; 415 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 9636.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 5.8%; Score 69.5; DB 4; Length 415;  
Best Local Similarity 20.9%; Pred. No. 87;  
RESULT 1415  
ID ADL12059 standard; protein; 415 AA.  
DE Drosophila dmtip1alt2 protein.  
PN W02003002137-A2.  
PD 09-JAN-2003.

PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
 Query Match 5.8%; Score 69.5; DB 7; Length 415;  
 Best Local Similarity 20.9%; Pred. No. 87;  
 RESULT 1416  
 ID ABB66992 standard; protein; 428 AA.  
 DE Drosophila melanogaster polypeptide SEQ ID NO 27768.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (BEKE-) PE CORP NY.  
 Query Match 5.8%; Score 69.5; DB 4; Length 428;  
 Best Local Similarity 20.9%; Pred. No. 91;  
 RESULT 1417  
 ID AD112058 standard; protein; 428 AA.  
 DE Drosophila dmtip1alt1 protein.  
 PN WO200302137-A2.  
 PD 09-JAN-2003.  
 PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.  
 Query Match 5.8%; Score 69.5; DB 7; Length 428;  
 Best Local Similarity 20.9%; Pred. No. 91;  
 RESULT 1418  
 ID AAY41284 standard; protein; 444 AA.  
 DE c1-NT-his fusion protein encoded by plasmid pLJM6-09.  
 PN WO995033-A1.  
 PD 21-OCT-1999.  
 PA (UYVA-) UNIV VANDERBILT.  
 Query Match 5.8%; Score 69.5; DB 2; Length 444;  
 Best Local Similarity 23.6%; Pred. No. 95;  
 RESULT 1419  
 ID AAG30875 standard; protein; 453 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36988.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match 5.8%; Score 69.5; DB 3; Length 453;  
 Best Local Similarity 23.3%; Pred. No. 98;  
 RESULT 1420  
 ID ADK47227 standard; protein; 453 AA.  
 DE Streptococcus pneumoniae protein, Seq ID No 3842.  
 PN US6699703-B1.  
 PD 02-MAR-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.8%; Score 69.5; DB 8; Length 453;  
 Best Local Similarity 24.4%; Pred. No. 98;  
 RESULT 1421  
 ID ADG95087 standard; protein; 461 AA.  
 DE Novel S. pneumoniae protein sequence, SEQ ID 3722.  
 PN US6800744-B1.  
 PD 05-OCT-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.8%; Score 69.5; DB 8; Length 461;  
 Best Local Similarity 24.4%; Pred. No. 1e+02;  
 RESULT 1422  
 ID ABA58957 standard; protein; 461 AA.  
 DE Streptococcus pneumoniae ORF amino acid sequence SEQ ID NO:3722.  
 PN US2005136404-A1.  
 PD 23-JUN-2005.  
 PA (DOUC/) DOUCETTE-STAMM L A.  
 PA (BUSH/) BUSH D.  
 Query Match 5.8%; Score 69.5; DB 9; Length 461;  
 Best Local Similarity 24.4%; Pred. No. 1e+02;  
 RESULT 1423  
 ID AAG30874 standard; protein; 476 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36987.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match 5.8%; Score 69.5; DB 3; Length 476;  
 Best Local Similarity 23.3%; Pred. No. 1e+02;  
 RESULT 1424  
 ID ADN22349 standard; protein; 477 AA.  
 DE Bacterial polypeptide #5002.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (HINK/) HINKLE G J.  
 Query Match 5.8%; Score 69.5; DB 6; Length 547;  
 Best Local Similarity 21.4%; Pred. No. 1.3e+02;  
 RESULT 1433

PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.8%; Score 69.5; DB 8; Length 477;  
 Best Local Similarity 23.5%; Pred. No. 1.1e+02;  
 RESULT 1425  
 ID ADS26512 standard; protein; 490 AA.  
 DE Bacterial polypeptide #17545.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.8%; Score 69.5; DB 8; Length 490;  
 Best Local Similarity 21.2%; Pred. No. 1.1e+02;  
 RESULT 1426  
 ID ABO61637 standard; protein; 494 AA.  
 DE Klebsiella pneumoniae polypeptide seqid 8154.  
 PN US6610836-B1.  
 PD 26-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.8%; Score 69.5; DB 7; Length 494;  
 Best Local Similarity 22.0%; Pred. No. 1.1e+02;  
 RESULT 1427  
 ID AAY41278 standard; protein; 500 AA.  
 DE Fusion protein containing rabbit prostaglandin EP2EP3 receptor.  
 PN WO995033-A1.  
 PD 21-OCT-1999.  
 PA (UYVA-) UNIV VANDERBILT.  
 Query Match 5.8%; Score 69.5; DB 2; Length 500;  
 Best Local Similarity 23.6%; Pred. No. 1.1e+02;  
 RESULT 1428  
 ID AAG30873 standard; protein; 503 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36986.  
 PN EPI033405-A2.  
 PD 06-SEP-2000.  
 Query Match 5.8%; Score 69.5; DB 3; Length 503;  
 Best Local Similarity 23.3%; Pred. No. 1.1e+02;  
 RESULT 1429  
 ID AAY92829 standard; protein; 535 AA.  
 DE C. pneumoniae CPN100557 processed antigen.  
 PN WO200024765-A2.  
 PD 04-MAY-2000.  
 PA (CONN-) CONNAUGHT LAB LTD.  
 Query Match 5.8%; Score 69.5; DB 3; Length 535;  
 Best Local Similarity 21.4%; Pred. No. 1.2e+02;  
 RESULT 1430  
 ID ADR13717 standard; protein; 540 AA.  
 DE Amidase, SEQ ID 54.  
 PN WO2004069848-A2.  
 PD 19-AUG-2004.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match 5.8%; Score 69.5; DB 8; Length 540;  
 Best Local Similarity 23.7%; Pred. No. 1.3e+02;  
 RESULT 1431  
 ID AAY92828 standard; protein; 547 AA.  
 DE C. pneumoniae CPN100557 antigen.  
 PN WO200024765-A2.  
 PD 04-MAY-2000.  
 PA (CONN-) CONNAUGHT LAB LTD.  
 Query Match 5.8%; Score 69.5; DB 3; Length 547;  
 Best Local Similarity 21.4%; Pred. No. 1.3e+02;  
 RESULT 1432  
 ID ABU26764 standard; protein; 547 AA.  
 DE Protein encoded by Prokaryotic essential gene #12291.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.8%; Score 69.5; DB 6; Length 547;  
 Best Local Similarity 21.4%; Pred. No. 1.3e+02;  
 RESULT 1433

ID ABU31940 standard; protein; 551 AA.  
DE Protein encoded by Prokaryotic essential gene #17467.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 551;  
Best Local Similarity 23.6%; Pred. No. 1.3e+02;  
RESULT 1434  
ID AAY01650 standard; protein; 557 AA.  
DE A protein with cation transporting activity.  
PN WO9913072-A1.  
PD 18-MAR-1999.  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
Query Match 5.8%; Score 69.5; DB 2; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
RESULT 1435  
ID AAY83929 standard; protein; 557 AA.  
DE Human carnitine transporter protein OCTN2.  
PN WO200014210-A1.  
PD 16-MAR-2000.  
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
Query Match 5.8%; Score 69.5; DB 3; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
RESULT 1436  
ID ABG03029 standard; protein; 557 AA.  
DE Novel human diagnostic protein #3020.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.8%; Score 69.5; DB 4; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
RESULT 1437  
ID ABB82979 standard; protein; 557 AA.  
DE Human SLC22A related protein-Genbank Identifier No. GI# 3242598.  
PN WO200299053-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
RESULT 1438  
ID ABB82980 standard; protein; 557 AA.  
DE Human SLC22A related protein-Genbank Identifier No. GI# 4507005.  
PN WO200299053-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
RESULT 1439  
ID ABO07242 standard; protein; 557 AA.  
DE Human p53 modifying protein, SEQ ID 202.  
PN WO200299122-A1.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
RESULT 1440  
ID ADE09321 standard; protein; 557 AA.  
DE Novel protein-related contig polypeptide sequence #387.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.8%; Score 69.5; DB 7; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
RESULT 1441  
ID ADE09261 standard; protein; 557 AA.  
DE Novel protein-related contig polypeptide sequence #327.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.8%; Score 69.5; DB 7; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
RESULT 1442  
ID ADP23817 standard; protein; 557 AA.

DE PRO polypeptide SEQ ID NO:995.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 5.8%; Score 69.5; DB 8; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
RESULT 1443  
ID ADY79867 standard; protein; 557 AA.  
DE Amino acid sequence of a human SLC22A5 polypeptide.  
PN WO2005026724-A2.  
PD 24-MAR-2005.  
PA (FARB-) BAYER HEALTHCARE AG.  
Query Match 5.8%; Score 69.5; DB 9; Length 557;  
Best Local Similarity 26.3%; Pred. No. 1.3e+02;  
RESULT 1444  
ID ADA34637 standard; protein; 559 AA.  
DE Acinetobacter baumannii protein #1798.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 6; Length 559;  
Best Local Similarity 20.2%; Pred. No. 1.3e+02;  
RESULT 1445  
ID ABO62908 standard; protein; 564 AA.  
DE Klebsiella pneumoniae polypeptide seqid 9425.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 7; Length 564;  
Best Local Similarity 23.6%; Pred. No. 1.3e+02;  
RESULT 1446  
ID ABB89665 standard; protein; 568 AA.  
DE Human polypeptide SEQ ID NO 2041.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.8%; Score 69.5; DB 5; Length 568;  
Best Local Similarity 22.4%; Pred. No. 1.3e+02;  
RESULT 1447  
ID ADB65515 standard; protein; 573 AA.  
DE Human protein encoded by clone TEST1120271790.  
PN EP1308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
Query Match 5.8%; Score 69.5; DB 7; Length 573;  
Best Local Similarity 22.7%; Pred. No. 1.4e+02;  
RESULT 1448  
ID ABB47410 standard; protein; 579 AA.  
DE Listeria monocytogenes protein #114.  
PN WO200177335-A2.  
PD 18-OCT-2001.  
PA (INSP-) INST PASTEUR.  
Query Match 5.8%; Score 69.5; DB 5; Length 579;  
Best Local Similarity 21.1%; Pred. No. 1.4e+02;  
RESULT 1449  
ID ABU32703 standard; protein; 579 AA.  
DE Protein encoded by Prokaryotic essential gene #18230.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELITR-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 579;  
Best Local Similarity 21.1%; Pred. No. 1.4e+02;  
RESULT 1450  
ID ABB65234 standard; protein; 599 AA.  
DE Hypoxia-regulated protein #108.  
PN WO200246465-A2.  
PD 13-JUN-2002.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Query Match 5.8%; Score 69.5; DB 5; Length 599;  
Best Local Similarity 19.6%; Pred. No. 1.4e+02;  
RESULT 1451  
ID AAE38584 standard; protein; 599 AA.

DE Human GAT1 GABA transporter protein.  
PN W02003061573-A2.  
PD 31-JUL-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 5.8%; Score 69.5; DB 7; Length 599;  
Best Local Similarity 19.6%; Pred. No. 1.4e+02;  
RESULT 1452  
ID ADD46025 standard; protein; 599 AA.  
DE Human Protein P30531, SEQ ID NO 11697.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 5.8%; Score 69.5; DB 7; Length 599;  
Best Local Similarity 19.6%; Pred. No. 1.4e+02;  
RESULT 1453  
ID AAY41285 standard; protein; 656 AA.  
DE CT-77A-TL fusion protein encoded by plasmid pLJM5-42T.  
PN W09953033-A1.  
PD 21-OCT-1999.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 5.8%; Score 69.5; DB 2; Length 656;  
Best Local Similarity 23.6%; Pred. No. 1.6e+02;  
RESULT 1454  
ID APP40194 standard; protein; 660 AA.  
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039.  
PN US6380370-B1.  
PD 30-APR-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 69.5; DB 5; Length 660;  
Best Local Similarity 27.2%; Pred. No. 1.7e+02;  
RESULT 1455  
ID AOS07250 standard; protein; 660 AA.  
DE Staphylococcus epidermis polypeptide seqid 6545.  
PN US2004147734-A1.  
PD 28-JUL-2004.  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
Query Match 5.8%; Score 69.5; DB 8; Length 660;  
Best Local Similarity 27.2%; Pred. No. 1.7e+02;  
RESULT 1456  
ID AAY17390 standard; protein; 663 AA.  
DE Human vesicle membrane protein-like protein 3.  
PN W09921994-A2.  
PD 06-MAY-1999.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 5.8%; Score 69.5; DB 2; Length 663;  
Best Local Similarity 22.0%; Pred. No. 1.7e+02;  
RESULT 1457  
ID ADM83092 standard; protein; 663 AA.  
DE Human vesicle membrane protein (VMP) 2.  
PN US2003175787-A1.  
PD 18-SEP-2003.  
PA (INCY-) INCYTE CORP.  
Query Match 5.8%; Score 69.5; DB 7; Length 663;  
Best Local Similarity 22.0%; Pred. No. 1.7e+02;  
RESULT 1458  
ID ADJ64317 standard; protein; 663 AA.  
DE Cartilage differentiation inhibiting protein, SEQ ID 12.  
PN W02004013326-A1.  
PD 12-FEB-2004.  
PA (ASAH) ASAH KASEI KK.  
Query Match 5.8%; Score 69.5; DB 8; Length 663;  
Best Local Similarity 22.0%; Pred. No. 1.7e+02;  
RESULT 1459  
ID ADO96536 standard; protein; 663 AA.  
DE T cell activation associated protein #357.  
PN W02004058805-A2.  
PD 15-JUL-2004.  
PA (ASAH-) ASAH KASEI PHARMA CORP.  
Query Match 5.8%; Score 69.5; DB 8; Length 663;  
Best Local Similarity 22.0%; Pred. No. 1.7e+02;  
RESULT 1460

ID ADY19824 standard; protein; 663 AA.  
DE PRO polypeptide SEQ ID NO 5630.  
PN W02005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 5.8%; Score 69.5; DB 9; Length 663;  
Best Local Similarity 22.0%; Pred. No. 1.7e+02;  
RESULT 1461  
ID ADY14394 standard; protein; 663 AA.  
DE PRO polypeptide SEQ ID NO 200.  
PN W02005016962-A2.  
PD 24-FEB-2005.  
PA (GETH) GENENTECH INC.  
Query Match 5.8%; Score 69.5; DB 9; Length 663;  
Best Local Similarity 22.0%; Pred. No. 1.7e+02;  
RESULT 1462  
ID ADO09827 standard; protein; 681 AA.  
DE Hamster SGLT homologue protein SEQ ID NO:50.  
PN W02004039405-A1.  
PD 13-MAY-2004.  
PA (TAKE) TAKEDA CHEM IND LTD.  
Query Match 5.8%; Score 69.5; DB 8; Length 681;  
Best Local Similarity 24.5%; Pred. No. 1.7e+02;  
RESULT 1463  
ID ABU41908 standard; protein; 695 AA.  
DE Protein encoded by Prokaryotic essential gene #27435.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 695;  
Best Local Similarity 24.3%; Pred. No. 1.8e+02;  
RESULT 1464  
ID ADJ48367 standard; protein; 764 AA.  
DE Maize oil-associated gene protein #26.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 5.8%; Score 69.5; DB 8; Length 764;  
Best Local Similarity 21.0%; Pred. No. 2e+02;  
RESULT 1465  
ID ABU43821 standard; protein; 801 AA.  
DE Protein encoded by Prokaryotic essential gene #29348.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.8%; Score 69.5; DB 6; Length 801;  
Best Local Similarity 19.9%; Pred. No. 2.2e+02;  
RESULT 1466  
ID AAY70245 standard; protein; 805 AA.  
DE Human Polycystin-L protein.  
PN W0200012046-A2.  
PD 09-MAR-2000.  
PA (BGMH) BRIGHAM & WOMENS HOSPITAL INC.  
Query Match 5.8%; Score 69.5; DB 3; Length 805;  
Best Local Similarity 20.4%; Pred. No. 2.2e+02;  
RESULT 1467  
ID ABB98140 standard; protein; 863 AA.  
DE Human PMM1 Incyte ID 7484157CD1.  
PN W0200246383-A2.  
PD 13-JUN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.8%; Score 69.5; DB 5; Length 863;  
Best Local Similarity 19.3%; Pred. No. 2.4e+02;  
RESULT 1468  
ID AAY96168 standard; protein; 877 AA.  
DE Saccharomyces cerevisiae OPT protein YPR194C.  
PN W0200052162-A2.  
PD 08-SEP-2000.  
PA (UYTE-) UNIV TENNESSEE RES CORP.

PA (BECK/) BECKER J M.  
PA (HAUS/) HAUSER M.  
PA (DOWN/) DONHARDT A.  
PA (BARR/) BARNES D.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 3; Length 877;  
PRED. NO. 2.5e+02;  
RESULT 1469  
ID ADS44117 standard; protein; 877 AA.  
DE Bacterial polypeptide #22547.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 8; Length 877;  
PRED. NO. 2.5e+02;  
RESULT 1470  
ID AAG70761 standard; protein; 881 AA.  
DE S cerevisiae apoptosis associated protein YUL197W.  
PN WO200102550-A2.  
PD 11-JAN-2001.  
PA (JANC/) JANSSEN PHARM NV.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 4; Length 881;  
PRED. NO. 2.5e+02;  
RESULT 1471  
ID ADZ26338 standard; protein; 913 AA.  
DE Mouse hypoxia-responsive gene CNGM0002 protein.  
PN WO2005033293-A2.  
PD 14-APR-2005.  
PA (CENZ/) CENTOCOR INC.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 9; Length 913;  
PRED. NO. 2.6e+02;  
RESULT 1472  
ID ABU16635 standard; protein; 1010 AA.  
DE Protein encoded by Prokaryotic essential gene #2162.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 6; Length 1010;  
PRED. NO. 3e+02;  
RESULT 1473  
ID ADA34462 standard; protein; 1028 AA.  
DE Acinetobacter baumannii protein #1633.  
PN US562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 6; Length 1028;  
PRED. NO. 3.1e+02;  
RESULT 1474  
ID AAM25671 standard; protein; 1684 AA.  
DE hABC3 protein.  
PN WO9702346-A2.  
PD 23-JAN-1997.  
PA (GENZ-) GENZYME CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 2; Length 1684;  
PRED. NO. 6.1e+02;  
RESULT 1475  
ID AAM46761 standard; protein; 1684 AA.  
DE Amino acid sequence of human ATP binding cassette transporter.  
PN WO9748797-A1.  
PD 24-DEC-1997.  
PA (GENZ-) GENZYME CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 2; Length 1684;  
PRED. NO. 6.1e+02;  
RESULT 1476  
ID AAM46771 standard; protein; 1704 AA.  
DE Amino acid sequence of human ATP binding cassette transporter.  
PN WO9748797-A1.  
PD 24-DEC-1997.  
PA (GENZ-) GENZYME CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 2; Length 1704;  
PRED. NO. 6.1e+02;

Best Local Similarity 20.3%; Pred. No. 6.2e+02;  
RESULT 1477  
ID ABP52094 standard; protein; 1704 AA.  
DE Homo sapiens ABC transporter ABCA3 protein SEQ ID NO:46.  
PN EP1217066-A1.  
PD 26-JUN-2002.  
PA (UYGE-) UNIV GENT.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 5; Length 1704;  
PRED. NO. 6.2e+02;  
RESULT 1478  
ID ADJ70414 standard; protein; 1704 AA.  
DE Human heat mitochondrial protein as a therapeutic target SegID2220.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 7; Length 1704;  
PRED. NO. 6.2e+02;  
RESULT 1479  
ID ADL61289 standard; protein; 1704 AA.  
DE Human ATP-binding cassette subfamily A (ABCI) member 3 protein.  
PN WO2004020583-A2.  
PD 11-MAR-2004.  
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 8; Length 1704;  
PRED. NO. 6.2e+02;  
RESULT 1480  
ID ADY70428 standard; protein; 1704 AA.  
DE Human beta-APP, ATP-binding cassette, subfamily A, member 3.  
PN WO2005023858-A1.  
PD 17-MAR-2005.  
PA (CELL-) CELLZOME AG.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 9; Length 1704;  
PRED. NO. 6.2e+02;  
RESULT 1481  
ID ADY70716 standard; protein; 1704 AA.  
DE Human nicotinyl-complex, ATP-binding cassette family A member 3 protein.  
PN WO2005023833-A2.  
PD 17-MAR-2005.  
PA (CELL-) CELLZOME AG.  
Query Match  
Best Local Similarity 5.8%; Score 69.5; DB 9; Length 1704;  
PRED. NO. 6.2e+02;  
RESULT 1482  
ID ADB09274 standard; protein; 154 AA.  
DE Allicoccocus ciliis antigenic protein SEQ ID NO:3214.  
PN WO2003048304-A2.  
PD 12-JUN-2003.  
PA (AMHP-) WYETH HOLDINGS CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69; DB 6; Length 154;  
PRED. NO. 25;  
RESULT 1483  
ID ADK16543 standard; protein; 178 AA.  
DE Nanocarhaeum egultans cancer-associated (CA) protein #247.  
PN WO2003039434-A2.  
PD 13-NOV-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69; DB 8; Length 178;  
PRED. NO. 31;  
RESULT 1484  
ID AAV65589 standard; protein; 191 AA.  
DE Propionibacterium acnes immunogenic protein #26485.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 5.8%; Score 69; DB 4; Length 191;  
PRED. NO. 34;  
RESULT 1485  
ID AAM62108 standard; protein; 191 AA.  
DE Propionibacterium acnes permease/transporter-related polypeptide #26784.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
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Query Match  
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OM protein - protein search, using sw model

Run on: May 12, 2006, 20:47:47 ; Search time 46 Seconds  
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Scoring table: BLOSUM62  
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Searched: 572060 seqs, 82675679 residues

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
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## SUMMARIES

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5	80.5	6.7	350 2 US-09-489-039A-9711	Sequence 9711, Ap
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7	79.5	6.7	406 2 US-09-171-699-4	Sequence 4, Appli
8	79.5	6.7	406 4 PCT-US94-02107-2	Sequence 2, Appli
9	79.5	6.7	723 2 US-09-976-594-503	Sequence 503, App
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138	71	5.9	471	2	US-09-170-496D-228	Sequence 228, Appl	211	69.5	5.8	599	1	US-08-501-722A-5	Sequence 5, Appl1
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249	68.5	5.7	225	2	US-09-543-681A-7698	Sequence 7698, Ap	322	68	5.7	471	2	US-08-423-752-14	Sequence 14, Appl
250	68.5	5.7	257	1	US-08-896-365-8	Sequence 8, Appli	323	68	5.7	471	2	US-08-716-873-8	Sequence 8, Appli
251	68.5	5.7	297	2	US-09-248-796A-20728	Sequence 20728, A	324	68	5.7	471	2	US-08-716-873-28	Sequence 28, Appl
252	68.5	5.7	327	2	US-09-161-994A-12	Sequence 12, Appl	325	68	5.7	471	2	US-09-368-431-8	Sequence 8, Appli
253	68.5	5.7	382	2	US-09-542-733-2	Sequence 2, Appli	326	68	5.7	471	2	US-09-368-431-28	Sequence 28, Appl
254	68.5	5.7	383	1	US-08-196-989B-4	Sequence 4, Appli	327	68	5.7	471	2	US-09-414-006-14	Sequence 14, Appl
255	68.5	5.7	383	1	US-08-760-936-4	Sequence 4, Appli	328	68	5.7	471	2	US-09-447-223-14	Sequence 14, Appl
256	68.5	5.7	383	1	US-08-760-936-4	Sequence 4, Appli	329	68	5.7	471	2	US-09-951-217-8	Sequence 8, Appli
257	68.5	5.7	417	2	US-09-225-024-4	Sequence 4, Appli	330	68	5.7	471	2	US-09-951-217-28	Sequence 28, Appl
258	68.5	5.7	437	2	US-09-134-000C-5002	Sequence 5002, Ap	331	68	5.7	471	2	US-09-792-024-88	Sequence 88, Appl
259	68.5	5.7	420	1	US-08-466-103A-2	Sequence 2, Appli	332	68	5.7	472	2	US-08-492-459-22	Sequence 22, Appl
260	68.5	5.7	437	2	US-09-328-352-102	Sequence 3,102, Ap	333	68	5.7	472	2	US-08-423-752-22	Sequence 22, Appl
261	68.5	5.7	444	2	US-08-482-746-15	Sequence 15, Appl	334	68	5.7	472	2	US-08-716-873-36	Sequence 36, Appl
262	68.5	5.7	444	2	US-09-580-734-15	Sequence 15, Appl	335	68	5.7	472	2	US-09-368-431-36	Sequence 36, Appl
263	68.5	5.7	444	2	US-08-374-009-15	Sequence 15, Appl	336	68	5.7	472	2	US-09-414-006-22	Sequence 22, Appl
264	68.5	5.7	444	2	US-09-191-724-15	Sequence 15, Appl	337	68	5.7	472	2	US-09-447-223-22	Sequence 22, Appl
265	68.5	5.7	444	2	US-09-631-603-11	Sequence 11, Appl	338	68	5.7	472	2	US-09-951-217-36	Sequence 36, Appl
266	68.5	5.7	448	1	US-08-811-897A-22	Sequence 22, Appl	339	68	5.7	480	1	US-08-440-103-22	Sequence 22, Appl
267	68.5	5.7	448	1	US-08-855-213-22	Sequence 22, Appl	340	68	5.7	480	1	US-08-440-542-22	Sequence 22, Appl
268	68.5	5.7	448	1	US-09-201-474-22	Sequence 22, Appl	341	68	5.7	480	1	US-08-221-368-22	Sequence 22, Appl
269	68.5	5.7	468	2	US-09-631-603-19	Sequence 19, Appl	342	68	5.7	480	1	US-08-440-210-22	Sequence 22, Appl
270	68.5	5.7	468	2	US-09-826-509-553	Sequence 553, App	343	68	5.7	480	2	US-09-046-604-22	Sequence 22, Appl
271	68.5	5.7	475	1	US-08-811-897A-26	Sequence 26, Appl	344	68	5.7	488	1	US-08-115-365-2	Sequence 2, Appli
272	68.5	5.7	475	1	US-08-855-213-26	Sequence 26, Appl	345	68	5.7	488	1	US-08-586-897-2	Sequence 2, Appli
273	68.5	5.7	476	1	US-09-201-474-26	Sequence 26, Appl	346	68	5.7	488	2	US-08-586-509-561	Sequence 561, App
274	68.5	5.7	476	1	US-08-811-897A-24	Sequence 24, Appl	347	68	5.7	503	1	US-08-484-840-4	Sequence 4, Appli
275	68.5	5.7	476	1	US-08-811-897A-28	Sequence 28, Appl	348	68	5.7	503	1	US-08-483-094-4	Sequence 4, Appli
276	68.5	5.7	476	1	US-08-855-213-24	Sequence 24, Appl	349	68	5.7	727	4	PCT-US94-05363A-2	Sequence 2, Appli
277	68.5	5.7	476	1	US-08-855-213-28	Sequence 28, Appl	350	68	5.7	859	2	US-09-538-092-206	Sequence 206, App
278	68.5	5.7	476	1	US-09-201-474-24	Sequence 24, Appl	351	68	5.7	908	2	US-08-823-110-1	Sequence 1, Appli
279	68.5	5.7	525	1	US-08-811-897A-23	Sequence 23, Appl	352	68	5.7	908	2	US-08-604-298-1	Sequence 1, Appli
280	68.5	5.7	525	1	US-08-855-213-23	Sequence 23, Appl	353	68	5.7	968	2	US-08-651-999A-7	Sequence 7, Appli
281	68.5	5.7	525	2	US-09-201-474-23	Sequence 23, Appl	354	68	5.7	968	2	US-09-385-752-7	Sequence 7, Appli
282	68.5	5.7	548	2	US-09-149-476-469	Sequence 469, App	355	68	5.7	968	2	US-09-949-016-5914	Sequence 5914, Ap
283	68.5	5.7	552	1	US-08-811-897A-27	Sequence 27, Appl	356	68	5.7	987	2	US-09-949-016-10358	Sequence 10369, A
284	68.5	5.7	552	1	US-08-855-213-27	Sequence 27, Appl	357	68	5.7	2013	1	US-08-384-977-12	Sequence 12, Appl
285	68.5	5.7	552	1	US-09-201-474-27	Sequence 27, Appl	358	68	5.7	2013	1	US-08-384-977-12	Sequence 12, Appl
286	68.5	5.7	553	1	US-08-811-897A-25	Sequence 25, Appl	359	68	5.7	2013	1	US-08-904-686A-12	Sequence 12, Appl
287	68.5	5.7	553	1	US-08-811-897A-29	Sequence 29, Appl	360	68	5.7	2013	1	US-08-904-686A-12	Sequence 12, Appl
288	68.5	5.7	553	1	US-08-855-213-25	Sequence 25, Appl	361	68	5.7	2620	1	US-08-324-977-32	Sequence 32, Appl
289	68.5	5.7	553	1	US-08-855-213-25	Sequence 25, Appl	362	68	5.7	2620	1	US-08-324-977-32	Sequence 32, Appl
290	68.5	5.7	553	1	US-08-855-213-25	Sequence 25, Appl	363	68	5.7	2620	1	US-08-324-977-32	Sequence 32, Appl
291	68.5	5.7	553	2	US-09-201-474-25	Sequence 25, Appl	364	68	5.7	2620	1	US-08-324-977-32	Sequence 32, Appl
292	68.5	5.7	553	2	US-09-201-474-29	Sequence 29, Appl	365	68	5.7	2620	1	US-08-324-977-32	Sequence 32, Appl
293	68.5	5.7	670	2	US-09-949-016-8907	Sequence 8907, Ap	366	68	5.7	2621	1	US-08-384-616-36	Sequence 36, Appl
294	68.5	5.7	738	2	US-09-252-991A-29885	Sequence 29885, A	367	68	5.7	2621	1	US-08-384-616-36	Sequence 36, Appl
295	68.5	5.7	738	2	US-09-107-532A-5096	Sequence 5096, Ap	368	68	5.7	2621	1	US-08-904-686A-36	Sequence 36, Appl
296	68.5	5.7	762	2	US-09-724-653-7	Sequence 7, Appli	369	68	5.7	2621	2	US-09-315-850-36	Sequence 36, Appl
297	68.5	5.7	1296	2	US-09-462-136-9	Sequence 9, Appli	370	68	5.7	3010	1	US-08-324-977-14	Sequence 14, Appl
298	68.5	5.7	188	2	US-09-270-767-36930	Sequence 36930, A	371	68	5.7	3010	1	US-08-324-977-14	Sequence 14, Appl
299	68.5	5.7	188	2	US-09-270-767-52147	Sequence 52147, A	372	68	5.7	3010	1	US-08-384-616-2	Sequence 2, Appli
300	68.5	5.7	247	2	US-09-603-208A-152	Sequence 152, App	373	68	5.7	3010	1	US-08-384-616-2	Sequence 2, Appli
301	68.5	5.7	258	2	US-09-053-197A-7	Sequence 7, Appli	374	68	5.7	3010	1	US-08-904-686A-2	Sequence 2, Appli
302	68.5	5.7	258	2	US-09-085-761A-7	Sequence 7, Appli	375	68	5.7	3010	1	US-08-904-686A-14	Sequence 14, Appl
303	68.5	5.7	309	2	US-09-328-352-6344	Sequence 6344, Ap	376	68	5.7	3010	2	US-09-315-850-2	Sequence 2, Appli
304	68.5	5.7	346	2	US-09-585-876-2	Sequence 2, Appli	377	68	5.7	3010	2	US-09-315-850-2	Sequence 2, Appli
305	68.5	5.7	346	2	US-09-979-603-2	Sequence 2, Appli	378	68	5.7	210	2	US-09-248-796A-20156	Sequence 20156, A
306	68.5	5.7	346	2	US-10-314-048A-14	Sequence 14, Appl	379	67.5	5.6	253	2	US-09-540-236-1093	Sequence 3093, Ap
307	68.5	5.7	346	2	US-10-314-048A-88	Sequence 88, Appl	380	67.5	5.6	305	2	US-09-252-991A-32461	Sequence 32461, A
308	68.5	5.7	355	1	US-08-012-988A-2	Sequence 2, Appli	381	67.5	5.6	345	2	US-09-979-603-18	Sequence 18, Appl
309	68.5	5.7	355	1	US-08-450-393A-5	Sequence 5, Appli	382	67.5	5.6	350	1	US-08-966-316-16	Sequence 16, Appl
310	68.5	5.7	355	2	US-08-446-669-5	Sequence 5, Appli	383	67.5	5.6	350	2	US-09-721-908-2	Sequence 2, Appli
311	68.5	5.7	355	2	US-09-239-938-1	Sequence 1, Appli	384	67.5	5.6	350	2	US-09-721-908-2	Sequence 2, Appli
312	68.5	5.7	355	2	US-09-886-319A-14	Sequence 14, Appl	385	67.5	5.6	457	2	US-09-543-681A-6044	Sequence 6044, Ap
313	68.5	5.7	355	2	US-10-039-659A-13	Sequence 13, Appl	386	67.5	5.6	457	2	US-09-543-681A-6044	Sequence 6044, Ap
314	68.5	5.7	355	2	US-09-961-068-1	Sequence 1, Appli	387	67.5	5.6	459	2	US-09-694-519-3	Sequence 3, Appli
315	68.5	5.7	355	2	US-09-625-573-5	Sequence 5, Appli	388	67.5	5.6	459	2	US-09-694-519-8	Sequence 8, Appli
316	68.5	5.7	355	2	US-09-960-547-1	Sequence 1, Appli	389	67.5	5.6	515	2	US-09-869-433-2	Sequence 2, Appli
317	68.5	5.7	373	2	PCT-US95-00476-5	Sequence 5, Appli	390	67.5	5.6	524	2	US-09-198-452A-369	Sequence 369, App
318	68.5	5.7	414	2	US-09-107-532A-7048	Sequence 7048, Ap	391	67.5	5.6	524	2	US-09-438-185A-353	Sequence 353, App
319	68.5	5.7	426	2	US-09-489-039A-10869	Sequence 10869, A	392	67.5	5.6	546	2	US-09-252-991A-17104	Sequence 17104, A

393	67.5	5.6	865	2	US-09-252-991A-18683	Sequence 18683, A
394	67.5	5.6	1334	1	US-08-811-897A-56	Sequence 56, Appl
395	67.5	5.6	1334	1	US-09-201-474-56	Sequence 56, Appl
396	67.5	5.6	1411	2	US-09-538-092-413	Sequence 413, Appl
397	67.5	5.6	2158	2	US-10-144-198-34	Sequence 34, Appl
398	67.5	5.6	2265	2	US-10-144-198-35	Sequence 35, Appl
399	67.5	5.6	2318	2	US-09-091-219-24	Sequence 24, Appl
400	67.5	5.6	2318	2	US-09-660-541-24	Sequence 24, Appl
401	67.5	5.6	2697	2	US-10-144-198-12	Sequence 12, Appl
402	67.5	5.6	3542	2	US-10-087-013-2	Sequence 2, Appl
403	67	5.6	133	2	US-09-198-452A-329	Sequence 329, Appl
404	67	5.6	153	2	US-09-438-185A-314	Sequence 314, Appl
405	67	5.6	159	2	US-09-134-000C-4969	Sequence 4969, Ap
406	67	5.6	164	2	US-09-902-540-13804	Sequence 13804, A
407	67	5.6	184	2	US-09-830-230A-150	Sequence 150, Appl
408	67	5.6	199	2	US-08-478-316-32	Sequence 32, Appl
409	67	5.6	199	2	US-09-019-793A-32	Sequence 32, Appl
410	67	5.6	200	1	US-08-131-625B-11	Sequence 11, Appl
411	67	5.6	200	2	US-08-301-435-15	Sequence 15, Appl
412	67	5.6	200	2	US-09-601-326-32	Sequence 32, Appl
413	67	5.6	200	4	PCT-US95-10904-15	Sequence 15, Appl
414	67	5.6	203	2	US-09-830-230A-149	Sequence 149, Appl
415	67	5.6	207	2	US-08-811-519-26	Sequence 26, Appl
416	67	5.6	222	2	US-09-270-767-37728	Sequence 37728, A
417	67	5.6	222	2	US-09-270-767-52945	Sequence 52945, A
418	67	5.6	282	2	US-09-270-767-35735	Sequence 35735, A
419	67	5.6	282	2	US-09-270-767-50952	Sequence 50952, A
420	67	5.6	295	2	US-09-372-422A-38	Sequence 38, Appl
421	67	5.6	300	2	US-09-107-532A-4523	Sequence 4523, Ap
422	67	5.6	449	2	US-09-769-787-110	Sequence 110, Appl
423	67	5.6	464	2	US-09-543-681A-6605	Sequence 18187, A
424	67	5.6	479	2	US-08-440-103-18	Sequence 6605, Ap
425	67	5.6	480	1	US-08-440-542-18	Sequence 18, Appl
426	67	5.6	480	1	US-08-231-368-18	Sequence 18, Appl
427	67	5.6	480	1	US-08-440-542-18	Sequence 18, Appl
428	67	5.6	480	1	US-08-440-210-18	Sequence 18, Appl
429	67	5.6	480	1	US-09-046-604-18	Sequence 18, Appl
430	67	5.6	496	2	US-10-146-704-3	Sequence 3, Appl1
431	67	5.6	635	2	US-10-104-047-2395	Sequence 2395, Ap
432	67	5.6	733	2	US-09-489-039A-7885	Sequence 7885, Ap
433	67	5.6	978	2	US-09-585-858-20	Sequence 20, Appl
434	67	5.6	978	2	US-10-270-878-20	Sequence 20, Appl
435	67	5.6	1093	2	US-09-248-796A-17108	Sequence 17108, A
436	67	5.6	1174	1	US-08-040-751-3	Sequence 3, Appl1
437	67	5.6	1174	1	US-08-291-368-2	Sequence 2, Appl1
438	67	5.6	1174	1	US-08-962-190-2	Sequence 2, Appl1
439	67	5.6	1174	4	PCT-US95-10310-72	Sequence 2, Appl1
440	67	5.6	1174	6	5164180-4	Patent No. 5164180
441	67	5.6	1242	1	US-08-680-326-33	Sequence 33, Appl
442	67	5.6	1242	2	US-09-904-065-12	Sequence 12, Appl
443	67	5.6	1242	2	US-09-904-065-13	Sequence 13, Appl
444	67	5.6	1511	2	US-09-487-558B-250	Sequence 250, Appl
445	67	5.6	3010	2	US-09-539-601-3	Sequence 3, Appl1
446	67	5.6	3010	2	US-09-539-601-21	Sequence 21, Appl
447	67	5.6	3010	2	US-09-539-601-37	Sequence 27, Appl
448	67	5.6	3010	2	US-09-539-601-33	Sequence 33, Appl
449	67	5.6	3287	1	US-08-477-451-7	Sequence 7, Appl1
450	66.5	5.6	197	2	US-09-134-000C-4925	Sequence 4925, Ap
451	66.5	5.6	200	2	US-08-686-968C-9	Sequence 9, Appl1
452	66.5	5.6	243	2	US-09-328-352-7321	Sequence 7321, Ap
453	66.5	5.6	288	1	US-08-466-103A-6	Sequence 6, Appl1
454	66.5	5.6	289	2	US-09-248-796A-17919	Sequence 17919, A
455	66.5	5.6	293	2	US-09-248-796A-18378	Sequence 18378, A
456	66.5	5.6	341	2	US-09-248-796A-18985	Sequence 18985, A
457	66.5	5.6	345	2	US-09-281-922-14	Sequence 14, Appl
458	66.5	5.6	359	2	US-09-828-523A-14	Sequence 14, Appl
459	66.5	5.6	370	2	US-09-828-523A-74	Sequence 74, Appl
460	66.5	5.6	384	2	US-09-949-016-6494	Sequence 6494, Ap
461	66.5	5.6	389	2	US-09-134-000C-3706	Sequence 3706, Ap
462	66.5	5.6	397	2	US-09-902-540-13316	Sequence 13316, A
463	66.5	5.6	413	2	US-09-328-352-5589	Sequence 5589, Ap
464	66.5	5.6	430	2	US-09-583-110-4230	Sequence 4230, Ap
465	66.5	5.6	437	2	US-09-107-433-3678	Sequence 3678, Ap
466	66.5	5.6	466	2	US-08-444-818-73	Sequence 73, Appl
467	66.5	5.6	467	2	US-09-248-796B-27314	Sequence 27314, A
468	66.5	5.6	468	1	US-08-440-103-14	Sequence 14, Appl
469	66.5	5.6	480	1	US-08-440-542-14	Sequence 14, Appl
470	66.5	5.6	480	1	US-08-231-368-14	Sequence 14, Appl
471	66.5	5.6	480	1	US-08-440-210-14	Sequence 14, Appl
472	66.5	5.6	480	1	US-09-046-604-14	Sequence 14, Appl
473	66.5	5.6	531	2	US-10-104-047-2775	Sequence 2775, Ap
474	66.5	5.6	537	2	US-09-489-039A-1149	Sequence 1149, A
475	66.5	5.6	550	1	US-08-121-057-4	Sequence 4, Appl1
476	66.5	5.6	550	1	US-08-509-187D-4	Sequence 4, Appl1
477	66.5	5.6	550	1	US-09-121-396-4	Sequence 4, Appl1
478	66.5	5.6	550	4	PCT-US93-09704A-4	Sequence 4, Appl1
479	66.5	5.6	557	2	US-09-248-796A-15455	Sequence 15455, A
480	66.5	5.6	627	2	US-09-328-352-4917	Sequence 4917, Ap
481	66.5	5.6	663	2	US-08-824-057-3	Sequence 3, Appl1
482	66.5	5.6	663	2	US-09-415-582-3	Sequence 3, Appl1
483	66.5	5.6	663	2	US-09-693-596-4	Sequence 4, Appl1
484	66.5	5.6	738	2	US-08-667-611-35	Sequence 35, Appl
485	66.5	5.6	738	2	US-09-690-359-35	Sequence 35, Appl
486	66.5	5.6	738	4	PCT-US92-06965A-5	Sequence 5, Appl1
487	66.5	5.6	750	2	US-09-949-016-7201	Sequence 7201, Ap
488	66.5	5.6	750	2	US-09-949-016-7202	Sequence 7202, Ap
489	66.5	5.6	801	2	US-09-710-279-90	Sequence 90, Appl
490	66.5	5.6	802	2	US-09-134-001C-3741	Sequence 3741, Ap
491	66.5	5.6	849	2	US-09-949-016-8846	Sequence 8846, Ap
492	66.5	5.6	849	2	US-09-949-016-8847	Sequence 8847, Ap
493	66.5	5.6	853	2	US-09-949-016-8275	Sequence 8275, Ap
494	66.5	5.6	853	2	US-09-949-016-8276	Sequence 8276, Ap
495	66.5	5.6	977	2	US-09-134-000C-5653	Sequence 5653, Ap
496	66.5	5.6	1897	2	US-09-792-024-98	Sequence 98, Appl
497	66.5	5.6	2261	2	US-08-444-818-66	Sequence 66, Appl
498	66.5	5.6	2884	1	US-08-466-975A-23	Sequence 23, Appl
499	66.5	5.6	2894	2	US-08-391-671A-23	Sequence 23, Appl
500	66.5	5.6	2894	2	US-08-467-902A-23	Sequence 23, Appl
501	66.5	5.6	2894	2	US-09-275-265-23	Sequence 23, Appl
502	66.5	5.6	2894	2	US-09-941-611-23	Sequence 23, Appl
503	66.5	5.6	2894	2	US-10-044-995-23	Sequence 23, Appl
504	66.5	5.6	2955	1	US-08-443-260-3	Sequence 3, Appl1
505	66.5	5.6	2955	2	US-08-443-800A-3	Sequence 3, Appl1
506	66.5	5.6	2955	2	US-08-443-900A-3	Sequence 3, Appl1
507	66.5	5.6	2955	2	US-08-444-818-124	Sequence 124, Appl
508	66.5	5.6	2955	2	US-08-249-843-3	Sequence 3, Appl1
509	66.5	5.6	2955	2	US-08-444-818-138	Sequence 138, Appl
510	66.5	5.6	3011	2	US-09-014-416-3	Sequence 3, Appl1
511	66.5	5.6	3011	1	US-08-440-103-36	Sequence 36, Appl
512	66.5	5.6	3011	1	US-08-440-542-36	Sequence 36, Appl
513	66.5	5.6	3011	1	US-07-910-750-10	Sequence 10, Appl
514	66.5	5.6	3011	1	US-08-440-519-10	Sequence 10, Appl
515	66.5	5.6	3011	1	US-08-231-368-36	Sequence 36, Appl
516	66.5	5.6	3011	1	US-08-440-210-36	Sequence 36, Appl
517	66.5	5.6	3011	1	US-08-833-678A-6	Sequence 6, Appl1
518	66.5	5.6	3011	2	US-08-444-818-177	Sequence 177, Appl
519	66.5	5.6	3011	2	US-09-014-416-5	Sequence 5, Appl1
520	66.5	5.6	3011	2	US-08-529-169A-6	Sequence 6, Appl1
521	66.5	5.6	3011	2	US-09-388-874-2	Sequence 2, Appl1
522	66.5	5.6	3011	2	US-09-046-604-36	Sequence 36, Appl
523	66.5	5.6	3011	2	US-08-440-549-10	Sequence 10, Appl
524	66.5	5.6	3011	2	US-08-850-328-1	Sequence 1, Appl1
525	66.5	5.6	3011	2	US-09-483-799-6	Sequence 6, Appl1
526	66.5	5.6	3011	2	US-09-16-359-2	Sequence 2, Appl1
527	66.5	5.6	3011	4	PCT-US91-02225-10	Sequence 10, Appl
528	66	5.5	192	2	US-09-270-767-61535	Sequence 61535, A
529	66	5.5	219	2	US-09-248-796A-15621	Sequence 15621, A
530	66	5.5	248	2	US-09-258-634-4	Sequence 4, Appl1
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532	66	5.5	289	2	US-09-134-001C-2917	Sequence 2917, Ap
533	66	5.5	329	2	US-09-107-532A-4973	Sequence 4973, Ap
534	66	5.5	316	2	US-09-328-352-6692	Sequence 6692, Ap
535	66	5.5	316	2	US-09-270-767-45996	Sequence 45996, A
536	66	5.5	370	2	US-09-172-353-7	Sequence 7, Appl1
537	66	5.5	370	2	US-08-776-971-140	Sequence 140, Appl
538	66	5.5	370	2	US-09-799-955-7	Sequence 7, Appl1

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540	66	5.5	370	2	US-09-716-147-140	Sequence 140, App	613	65	5.4	375	2	US-09-799-978-6	Sequence 6, Appli
541	66	5.5	381	1	US-08-845-566-3	Sequence 3, Appli	614	65	5.4	401	2	US-09-799-978-8	Sequence 8, Appli
542	66	5.5	381	1	US-08-467-948A-28	Sequence 28, Appli	615	65	5.4	415	1	US-08-110-286A-2	Sequence 2, Appli
543	66	5.5	381	2	US-08-852-824-18	Sequence 18, Appli	616	65	5.4	415	2	US-08-482-746-2	Sequence 2, Appli
544	66	5.5	381	2	US-08-467-947A-28	Sequence 28, Appli	617	65	5.4	415	2	US-09-580-734-2	Sequence 2, Appli
545	66	5.5	381	2	US-09-731-030A-17	Sequence 17, Appli	618	65	5.4	415	2	US-08-374-009-2	Sequence 2, Appli
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548	66	5.5	402	2	US-09-799-978-38	Sequence 38, Appli	621	65	5.4	415	2	US-09-799-978-4	Sequence 4, Appli
549	66	5.5	412	2	US-10-138-701-59	Sequence 59, Appli	622	65	5.4	415	2	US-09-826-509-483	Sequence 483, App
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551	66	5.5	447	2	US-09-825-923-2	Sequence 2, Appli	624	65	5.4	441	2	US-09-540-236-2016	Sequence 2016, Ap
552	66	5.5	450	2	US-09-825-923-4	Sequence 4, Appli	625	65	5.4	441	2	US-08-572-814D-2	Sequence 2, Appli
553	66	5.5	582	2	US-09-721-870-179	Sequence 179, App	626	65	5.4	461	1	US-09-333-696-2	Sequence 2, Appli
554	66	5.5	583	2	US-09-270-767-38131	Sequence 38131, A	627	65	5.4	461	2	US-09-333-696-2	Sequence 2, Appli
555	66	5.5	583	2	US-09-270-767-53348	Sequence 53348, A	628	65	5.4	461	2	US-09-282-218A-2	Sequence 2, Appli
556	66	5.5	1250	2	US-08-938-291A-9	Sequence 9, Appli	629	65	5.4	463	2	US-08-612-973-46	Sequence 46, Appli
557	66	5.5	1250	2	US-09-589-619-9	Sequence 9, Appli	630	65	5.4	463	2	US-08-927-597-46	Sequence 46, Appli
558	65.5	145	145	2	US-09-134-000C-3453	Sequence 3453, Ap	631	65	5.4	463	2	US-08-927-597-46	Sequence 46, Appli
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561	65.5	5.5	210	2	US-09-538-092-121	Sequence 121, App	634	65	5.4	490	2	US-08-928-757-36	Sequence 7, Appli
562	65.5	5.5	210	2	US-09-487-558B-320	Sequence 320, App	635	65	5.4	491	2	US-09-181-339-7	Sequence 11239, A
563	65.5	5.5	291	2	US-09-252-991A-32938	Sequence 32938, A	636	65	5.4	516	2	US-09-949-016-11239	Sequence 5869, Ap
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566	65.5	5.5	369	2	US-09-799-955-6	Sequence 6, Appli	639	65	5.4	632	2	US-08-928-757-48	Sequence 50, Appli
567	65.5	5.5	369	2	US-09-170-496D-26	Sequence 170, App	640	65	5.4	632	2	US-08-928-757-50	Sequence 50, Appli
568	65.5	5.5	369	2	US-09-170-496D-178	Sequence 178, App	641	65	5.4	809	2	US-08-927-597-50	Sequence 50, Appli
569	65.5	5.5	407	2	US-09-252-991A-21511	Sequence 21511, A	642	65	5.4	809	2	US-08-928-757-50	Sequence 5138, Ap
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571	65.5	5.5	468	2	US-09-252-991A-17314	Sequence 17314, A	644	65	5.4	5069	2	US-10-042-665A-5	Sequence 3730, Ap
572	65.5	5.5	487	2	US-09-583-110-4658	Sequence 4658, Ap	645	65	5.4	215	2	US-09-107-532A-3730	Sequence 9, Appli
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575	65.5	5.5	563	2	US-09-248-796A-15726	Sequence 15726, A	648	65	5.4	311	2	US-09-328-352-7066	Sequence 17395, A
576	65.5	5.5	630	2	US-09-342-647-2	Sequence 2, Appli	649	65	5.4	311	2	US-09-328-352-7066	Sequence 17395, A
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579	65.5	5.5	860	2	US-08-485-128-4	Sequence 4, Appli	652	65	5.4	344	1	US-08-726-575A-2	Sequence 644, App
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581	65.5	5.5	860	2	US-09-824-637-4	Sequence 4, Appli	654	65	5.4	349	2	US-09-134-001C-4519	Sequence 4519, Ap
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584	65.5	5.5	1226	1	US-08-540-804-12	Sequence 12, Appli	657	65	5.4	394	2	US-09-107-433-3892	Sequence 3892, Ap
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587	65.5	5.5	1226	2	US-08-521-872-12	Sequence 12, Appli	660	65	5.4	407	2	US-09-328-352-5605	Sequence 5605, Ap
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589	65.5	5.5	1410	2	US-09-037-188-4	Sequence 4, Appli	662	65	5.4	411	4	PCT-US95-06725-2	Sequence 7, Appli
590	65.5	5.5	1410	2	US-09-285-310-4	Sequence 4, Appli	663	65	5.4	411	4	US-09-799-978-32	Sequence 32, Appli
591	65.5	5.5	1410	2	US-09-753-385-4	Sequence 4, Appli	664	65	5.4	418	4	PCT-US94-01321-72	Sequence 72, Appli
592	65.5	5.5	1427	2	US-09-487-558B-354	Sequence 354, App	665	65	5.4	437	2	US-09-353-332-2	Sequence 2, Appli
593	65	5.5	1267	2	US-09-107-532A-3813	Sequence 3813, Ap	666	65	5.4	444	2	US-10-098-600B-33	Sequence 33, Appli
594	65	5.4	181	2	US-09-126-640-10	Sequence 10, Appli	667	65	5.4	446	1	US-07-781-254A-3	Sequence 2, Appli
595	65	5.4	181	2	US-09-288-292A-10	Sequence 10, Appli	668	65	5.4	446	1	US-07-781-254A-3	Sequence 3, Appli
596	65	5.4	182	2	US-08-826-246-8	Sequence 8, Appli	669	65	5.4	446	1	US-09-252-991A-20563	Sequence 20563, A
597	65	5.4	182	2	US-08-944-495-8	Sequence 8, Appli	670	65	5.4	447	2	US-09-855-213-19	Sequence 19, Appli
598	65	5.4	182	2	US-08-925-588-8	Sequence 8, Appli	671	65	5.4	448	1	US-08-811-697A-18	Sequence 18, Appli
599	65	5.4	182	2	US-09-372-044-8	Sequence 8, Appli	672	65	5.4	448	1	US-08-855-213-18	Sequence 18, Appli
600	65	5.4	182	2	US-08-825-486-8	Sequence 8, Appli	673	65	5.4	448	2	US-09-201-474-18	Sequence 18, Appli
601	65	5.4	193	2	US-08-826-248-8	Sequence 8, Appli	674	65	5.4	464	2	US-09-532A-5509	Sequence 5509, Ap
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603	65	5.4	223	2	US-10-162-012-9	Sequence 9, Appli	676	65	5.4	467	2	US-08-855-213-19	Sequence 19, Appli
604	65	5.4	278	2	US-09-949-016-8160	Sequence 8160, Ap	677	65	5.4	475	1	US-08-811-697A-20	Sequence 20, Appli
605	65	5.4	282	2	US-09-107-532A-5538	Sequence 5538, Ap	678	65	5.4	476	1	US-08-855-213-20	Sequence 20, Appli
606	65	5.4	311	2	US-09-252-991A-19489	Sequence 19489, A	679	65	5.4	476	2	US-09-201-474-20	Sequence 20, Appli
607	65	5.4	322	2	US-09-538-092-506	Sequence 506, App	680	65	5.4	482	2	US-09-107-532A-4512	Sequence 4512, Ap
608	65	5.4	336	2	US-09-095-163-2	Sequence 2, Appli	681	65	5.4	482	2	US-09-134-000C-4234	Sequence 4234, Ap
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610	65	5.4	362	2	US-09-503-565-6	Sequence 6, Appli	683	65	5.4	487	2	US-09-949-016-9649	Sequence 9649, Ap
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686	64.5	5.4	494	2	US-09-299-549-5	Sequence 5, Appl1	759	64	5.4	3011	4	PCT-US93-00907-1	Sequence 1, Appl1
687	64.5	5.4	494	2	US-09-610-417-5	Sequence 5, Appl1	760	64	5.4	3011	4	PCT-US94-07280-1	Sequence 1, Appl1
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690	64.5	5.4	495	1	US-08-855-213-21	Sequence 21, Appl1	763	63.5	5.3	118	2	US-09-627-376-17	Sequence 17, Appl1
691	64.5	5.4	495	1	US-09-201-474-21	Sequence 21, Appl1	764	63.5	5.3	124	2	US-09-270-767-50046	Sequence 34829, A
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695	64.5	5.4	557	2	US-10-172-527A-7	Sequence 7, Appl1	768	63.5	5.3	219	2	US-09-107-433-3794	Sequence 3794, Ap
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697	64.5	5.4	576	2	US-08-948-564-16	Sequence 16, Appl1	770	63.5	5.3	253	2	US-09-602-787A-8	Sequence 8, Appl1
698	64.5	5.4	747	2	US-09-291-922-2	Sequence 2, Appl1	771	63.5	5.3	254	2	US-09-489-039A-9738	Sequence 9738, Ap
699	64.5	5.4	757	2	US-09-585-858-24	Sequence 24, Appl1	772	63.5	5.3	275	1	US-08-118-270-66	Sequence 66, Appl1
700	64.5	5.4	757	2	US-10-270-878-24	Sequence 24, Appl1	773	63.5	5.3	275	2	PCT-US93-08528-66	Sequence 66, Appl1
701	64.5	5.4	795	2	US-09-107-532A-5429	Sequence 5429, Ap	774	63.5	5.3	279	2	US-09-134-001C-4667	Sequence 4667, Ap
702	64.5	5.4	2146	2	US-09-949-016-6947	Sequence 6947, Ap	775	63.5	5.3	280	1	US-08-781-562-4	Sequence 4, Appl1
703	64.5	5.4	3033	1	US-07-925-695-8	Sequence 8, Appl1	776	63.5	5.3	308	2	US-09-252-991A-18800	Sequence 18800, A
704	64	5.4	106	2	US-09-270-767-41157	Sequence 41157, A	777	63.5	5.3	337	2	US-10-114-048A-28	Sequence 28, Appl1
705	64	5.4	106	2	US-09-270-767-56373	Sequence 56373, A	778	63.5	5.3	342	2	US-09-116-498A-4	Sequence 4, Appl1
706	64	5.4	168	2	US-09-543-681A-6129	Sequence 6129, Ap	779	63.5	5.3	342	2	US-09-116-498A-4	Sequence 4, Appl1
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708	64	5.4	216	2	US-09-270-767-46297	Sequence 46297, A	781	63.5	5.3	342	2	US-09-852-156-4	Sequence 6, Appl1
709	64	5.4	284	2	US-09-270-767-37726	Sequence 37726, A	782	63.5	5.3	349	2	US-09-452-991A-24644	Sequence 24644, A
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711	64	5.4	285	2	US-09-248-796A-14187	Sequence 14187, A	784	63.5	5.3	358	2	US-09-270-767-41449	Sequence 41449, A
712	64	5.4	296	2	US-09-100-804-12	Sequence 12, Appl1	785	63.5	5.3	362	1	US-09-933-999A-5	Sequence 5, Appl1
713	64	5.4	335	2	US-09-107-532A-4900	Sequence 4900, Ap	786	63.5	5.3	372	1	US-08-302-056-5	Sequence 5, Appl1
714	64	5.4	336	2	US-09-848-294-5	Sequence 5, Appl1	787	63.5	5.3	372	1	US-08-076-093A-6	Sequence 6, Appl1
715	64	5.4	357	2	US-08-688-988-28	Sequence 28, Appl1	788	63.5	5.3	372	1	US-08-701-265-6	Sequence 6, Appl1
716	64	5.4	357	2	US-09-489-039A-10505	Sequence 10505, A	789	63.5	5.3	372	1	US-08-284-586-6	Sequence 6, Appl1
717	64	5.4	363	2	US-09-248-796A-19011	Sequence 19011, A	790	63.5	5.3	372	1	US-08-805-478-6	Sequence 6, Appl1
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719	64	5.4	367	2	US-09-134-001C-4082	Sequence 4082, Ap	792	63.5	5.3	372	1	US-08-801-238-6	Sequence 6, Appl1
720	64	5.4	411	1	US-08-381-433A-4	Sequence 4, Appl1	793	63.5	5.3	372	1	US-08-801-238-6	Sequence 6, Appl1
721	64	5.4	411	1	US-08-981-189B-12	Sequence 18, Appl1	794	63.5	5.3	372	1	US-09-104-296-6	Sequence 6, Appl1
722	64	5.4	411	2	US-09-799-978-18	Sequence 4, Appl1	795	63.5	5.3	372	2	US-08-982-493-8	Sequence 8, Appl1
723	64	5.4	411	2	US-09-881-401-4	Sequence 4, Appl1	796	63.5	5.3	372	2	US-09-170-496D-66	Sequence 66, Appl1
724	64	5.4	412	2	US-09-489-039A-8361	Sequence 8361, Ap	797	63.5	5.3	372	2	US-09-170-496D-66	Sequence 66, Appl1
725	64	5.4	413	2	US-09-491-577-72	Sequence 72, Appl1	798	63.5	5.3	372	2	US-09-170-496D-66	Sequence 66, Appl1
726	64	5.4	416	2	US-09-540-236-2393	Sequence 2393, Ap	799	63.5	5.3	379	2	US-09-248-796A-14491	Sequence 14491, A
727	64	5.4	420	2	US-09-583-447A-6	Sequence 6, Appl1	800	63.5	5.3	379	2	US-09-583-447A-6	Sequence 6, Appl1
728	64	5.4	431	2	US-08-981-189B-13	Sequence 13, Appl1	801	63.5	5.3	404	2	US-09-107-433-3747	Sequence 3747, Ap
729	64	5.4	431	2	US-09-799-978-20	Sequence 20, Appl1	802	63.5	5.3	406	2	US-09-252-991A-26429	Sequence 26429, A
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731	64	5.4	440	2	US-09-252-991A-23910	Sequence 23910, A	804	63.5	5.3	416	2	US-09-328-352-4300	Sequence 4300, Ap
732	64	5.4	469	2	US-09-328-352-4250	Sequence 4250, Ap	805	63.5	5.3	428	2	US-09-799-978-36	Sequence 36, Appl1
733	64	5.4	489	1	US-09-062-890-38	Sequence 38, Appl1	806	63.5	5.3	437	2	US-09-949-016-8094	Sequence 8094, Ap
734	64	5.4	501	2	US-09-902-540-11195	Sequence 11195, A	807	63.5	5.3	446	1	US-08-672-814D-11	Sequence 11, Appl1
735	64	5.4	501	2	US-09-583-447A-2	Sequence 2, Appl1	808	63.5	5.3	446	2	US-09-333-696-11	Sequence 11, Appl1
736	64	5.4	504	2	US-09-583-447A-4	Sequence 4, Appl1	809	63.5	5.3	446	2	US-09-282-218A-19	Sequence 19, Appl1
737	64	5.4	534	2	US-09-710-279-920	Sequence 920, App	810	63.5	5.3	458	2	US-09-252-991A-20655	Sequence 20655, A
738	64	5.4	535	2	US-09-343-681A-4582	Sequence 4582, Ap	811	63.5	5.3	444	2	US-09-489-039A-10432	Sequence 10432, A
739	64	5.4	586	2	US-09-040-725A-1	Sequence 1, Appl1	812	63.5	5.3	453	1	US-08-194-338-7	Sequence 7, Appl1
740	64	5.4	686	2	US-09-134-000C-5066	Sequence 5066, Ap	813	63.5	5.3	459	2	US-09-991-181-138	Sequence 138, App
741	64	5.4	757	2	US-09-585-858-23	Sequence 23, Appl1	814	63.5	5.3	459	2	US-09-990-444-138	Sequence 138, App
742	64	5.4	757	2	US-10-270-878-23	Sequence 23, Appl1	815	63.5	5.3	459	2	US-09-997-333-138	Sequence 138, App
743	64	5.4	967	1	US-08-188-281B-13	Sequence 13, Appl1	816	63.5	5.3	458	2	US-09-992-598A-138	Sequence 138, App
744	64	5.4	967	4	PCT-US94-07280-13	Sequence 13, Appl1	817	63.5	5.3	458	2	US-09-543-681A-4949	Sequence 4949, Ap
745	64	5.4	967	4	PCT-US95-01087-13	Sequence 13, Appl1	818	63.5	5.3	458	2	US-09-469-200E-10	Sequence 10, Appl1
746	64	5.4	1116	2	US-07-543-681A-4379	Sequence 4379, Ap	819	63.5	5.3	358	2	US-09-637-755A-89	Sequence 89, Appl1
747	64	5.4	1462	2	US-07-792-600-11	Sequence 11, Appl1	820	63.5	5.3	759	1	US-08-811-871A-89	Sequence 89, Appl1
748	64	5.4	1462	2	US-09-157-021-31	Sequence 31, Appl1	821	63.5	5.3	759	2	US-09-201-945-89	Sequence 89, Appl1
749	64	5.4	1462	2	US-09-156-842-31	Sequence 31, Appl1	822	63.5	5.3	866	2	US-08-651-999A-1	Sequence 1, Appl1
750	64	5.4	1462	2	US-09-591-514-11	Sequence 11, Appl1	823	63.5	5.3	866	2	US-09-385-752-1	Sequence 1, Appl1
751	64	5.4	1648	1	PCT-US94-07280-12	Sequence 12, Appl1	824	63.5	5.3	979	2	US-10-104-047-2446	Sequence 2446, Ap
752	64	5.4	1648	4	PCT-US95-01087-12	Sequence 12, Appl1	825	63.5	5.3	2080	2	US-09-382-552-2	Sequence 2, Appl1
753	64	5.4	2436	4	US-08-444-818-89	Sequence 89, Appl1	826	63	5.3	1477	2	US-09-270-767-45186	Sequence 45186, A
754	64	5.4	2772	2	US-08-444-818-89	Sequence 89, Appl1	827	63	5.3	177	2	US-09-492-1068A-20	Sequence 20, Appl1
755	64	5.4	3011	1	US-08-188-281B-1	Sequence 1, Appl1	828	63	5.3	180	2	US-09-107-532A-5495	Sequence 5495, Ap
756	64	5.4	3011	1	US-08-453-552-1	Sequence 1, Appl1	829	63	5.3	197	2	US-09-198-452A-403	Sequence 403, App
757	64	5.4	3011	1	US-08-453-552-1	Sequence 1, Appl1	830	63	5.3	218	2	US-09-134-000C-4489	Sequence 4489, Ap



831	63	5.3	233	2	US-09-134-001C-4013	Sequence 4013, Ap	904	62.5	5.2	255	2	US-09-992-598-287	Sequence 287, App
832	63	5.3	240	2	US-09-252-991A-2976	Sequence 2976, A	905	62.5	5.2	261	2	US-09-328-352-6619	Sequence 6619, Ap
833	63	5.3	245	2	US-09-949-016-11068	Sequence 11068, A	906	62.5	5.2	304	2	US-09-352-991A-22398	Sequence 22398, A
834	63	5.3	258	2	US-09-830-807-13	Sequence 13, Appl	907	62.5	5.2	304	2	US-09-107-532A-4681	Sequence 4681, Ap
835	63	5.3	259	2	US-09-261-5998-3	Sequence 3, Appl	908	62.5	5.2	337	1	US-08-926-724-1	Sequence 1, Appl
836	63	5.3	259	2	US-09-456-455A-3	Sequence 3, Appl	909	62.5	5.2	337	1	US-09-949-016-6562	Sequence 6562, Ap
837	63	5.3	264	2	US-09-270-767-11787	Sequence 41787, A	910	62.5	5.2	341	2	US-09-252-991A-30051	Sequence 30051, A
838	63	5.3	264	2	US-09-583-110-41171	Sequence 41171, Ap	911	62.5	5.2	342	2	US-09-134-000C-5123	Sequence 5123, Ap
839	63	5.3	295	2	US-09-107-532A-5499	Sequence 5499, Ap	912	62.5	5.2	343	2	US-09-743-871B-1	Sequence 1, Appl
840	63	5.3	359	2	US-09-134-001C-3246	Sequence 3246, Ap	913	62.5	5.2	343	2	US-09-743-871B-1	Sequence 5, Appl
841	63	5.3	359	2	US-08-688-988-12	Sequence 32, Appl	914	62.5	5.2	345	2	US-09-543-681A-4410	Sequence 4410, Ap
842	63	5.3	361	1	US-08-390-162-4	Sequence 4, Appl	915	62.5	5.2	349	2	US-09-162-524-3	Sequence 3, Appl
843	63	5.3	361	1	US-08-685-945B-4	Sequence 4, Appl	916	62.5	5.2	349	2	US-09-762-661A-2	Sequence 2, Appl
844	63	5.3	365	1	US-08-390-162-2	Sequence 2, Appl	917	62.5	5.2	352	2	US-09-829-275-5	Sequence 5, Appl
845	63	5.3	365	1	US-08-685-945B-2	Sequence 2, Appl	918	62.5	5.2	353	2	US-09-949-016-8077	Sequence 8077, Ap
846	63	5.3	366	1	US-09-107-433-5158	Sequence 5158, Ap	919	62.5	5.2	367	2	US-09-830-807-26	Sequence 26, Appl
847	63	5.3	370	2	US-09-172-353-2	Sequence 2, Appl	920	62.5	5.2	383	4	PCT-US94-01321-2	Sequence 8, Appl
848	63	5.3	370	2	US-09-172-353-3	Sequence 3, Appl	921	62.5	5.2	383	4	PCT-US94-01321-2	Sequence 2, Appl
849	63	5.3	370	2	US-09-799-985-2	Sequence 2, Appl	922	62.5	5.2	432	2	US-09-489-039A-7223	Sequence 7223, Ap
850	63	5.3	370	2	US-09-799-985-3	Sequence 3, Appl	923	62.5	5.2	434	2	US-09-198-452A-434	Sequence 434, App
851	63	5.3	380	2	US-09-710-279-2426	Sequence 2426, Ap	924	62.5	5.2	434	2	US-09-438-185A-417	Sequence 417, App
852	63	5.3	384	2	US-09-134-001C-3437	Sequence 3437, Ap	925	62.5	5.2	439	2	US-09-489-039A-13336	Sequence 1336, A
853	63	5.3	388	2	US-09-940-921B-7	Sequence 7, Appl	926	62.5	5.2	441	2	US-09-248-796A-16114	Sequence 16114, A
854	63	5.3	415	2	US-08-482-746-13	Sequence 13, Appl	927	62.5	5.2	442	2	US-08-121-446-4	Sequence 4, Appl
855	63	5.3	415	2	US-09-580-734-13	Sequence 13, Appl	928	62.5	5.2	442	2	US-09-520-210-10	Sequence 10, Appl
856	63	5.3	415	2	US-08-374-009-13	Sequence 13, Appl	929	62.5	5.2	442	2	US-09-826-509-497	Sequence 497, App
857	63	5.3	415	2	US-09-191-724-13	Sequence 13, Appl	930	62.5	5.2	443	2	US-09-161-994A-3	Sequence 3, Appl
858	63	5.3	415	2	US-09-799-978-22	Sequence 22, Appl	931	62.5	5.2	444	2	US-10-098-600B-36	Sequence 36, Appl
859	63	5.3	422	2	US-09-625-188-12	Sequence 12, Appl	932	62.5	5.2	452	1	US-08-117-361C-1	Sequence 1, Appl
860	63	5.3	431	1	US-08-381-433A-2	Sequence 2, Appl	933	62.5	5.2	452	1	US-09-710-279-1834	Sequence 1834, Ap
861	63	5.3	441	2	US-09-489-039A-10091	Sequence 10091, A	934	62.5	5.2	453	2	US-09-489-039A-10468	Sequence 10468, A
862	63	5.3	450	1	US-08-194-338-5	Sequence 5, Appl	935	62.5	5.2	453	2	US-09-769-863A-14	Sequence 14, Appl
863	63	5.3	450	1	US-08-444-734A-8	Sequence 8, Appl	936	62.5	5.2	459	2	US-09-489-039A-9027	Sequence 9027, Ap
864	63	5.3	451	1	US-09-134-001C-4420	Sequence 4420, Ap	937	62.5	5.2	463	2	US-09-134-001C-3973	Sequence 3973, Ap
865	63	5.3	489	1	US-09-062-8890-34	Sequence 34, Appl	938	62.5	5.2	476	2	US-09-489-039A-13346	Sequence 13346, A
866	63	5.3	489	1	US-09-062-8890-36	Sequence 36, Appl	939	62.5	5.2	480	2	US-09-489-039A-13045	Sequence 13045, A
867	63	5.3	508	2	US-10-314-048A-16	Sequence 16, Appl	940	62.5	5.2	516	2	US-09-949-002-526	Sequence 526, App
868	63	5.3	508	2	US-10-314-048A-92	Sequence 92, Appl	941	62.5	5.2	533	2	US-09-769-867-60	Sequence 60, Appl
869	63	5.3	509	1	US-08-890-980-2	Sequence 2, Appl	942	62.5	5.2	539	2	US-09-916-6363	Sequence 6363, Ap
870	63	5.3	509	2	US-08-890-979-2	Sequence 2, Appl	943	62.5	5.2	541	2	US-09-158-767-19	Sequence 19, Appl
871	63	5.3	509	2	US-09-033-894-2	Sequence 2, Appl	944	62.5	5.2	541	2	US-09-158-767-20	Sequence 20, Appl
872	63	5.3	509	2	US-09-031-626-2	Sequence 2, Appl	945	62.5	5.2	541	2	US-09-713-794-19	Sequence 19, Appl
873	63	5.3	509	2	US-09-054-272-55	Sequence 55, Appl	946	62.5	5.2	541	2	US-09-713-794-20	Sequence 20, Appl
874	63	5.3	640	2	US-09-252-991A-77542	Sequence 27542, A	947	62.5	5.2	557	1	US-08-424-788-6	Sequence 6, Appl
875	63	5.3	692	2	US-09-540-236-3150	Sequence 3150, Ap	948	62.5	5.2	578	1	US-08-424-788-5	Sequence 5, Appl
876	63	5.3	729	2	US-09-291-922-29	Sequence 29, Appl	949	62.5	5.2	578	1	US-08-110-683-2	Sequence 2, Appl
877	63	5.3	795	2	US-09-252-991A-19085	Sequence 19085, A	950	62.5	5.2	578	1	US-08-683-743-2	Sequence 2, Appl
878	63	5.3	822	2	US-08-684-932A-38	Sequence 38, Appl	951	62.5	5.2	578	1	US-08-472-097-2	Sequence 2, Appl
879	63	5.3	822	2	US-09-618-304B-2	Sequence 2, Appl	952	62.5	5.2	578	1	US-08-472-097-2	Sequence 2, Appl
880	63	5.3	926	2	US-10-314-048A-104	Sequence 104, App	953	62.5	5.2	578	2	US-09-439-672-2	Sequence 2, Appl
881	63	5.3	943	1	US-08-469-537A-107	Sequence 107, App	954	62.5	5.2	578	2	US-09-949-002-322	Sequence 322, App
882	63	5.3	1027	2	US-09-903-540-11750	Sequence 11750, A	955	62.5	5.2	578	4	PCT-US93-11638-2	Sequence 2, Appl
883	63	5.3	1802	2	US-09-322-478-18	Sequence 18, Appl	956	62.5	5.2	605	2	US-09-328-532A-7890	Sequence 7890, Ap
884	63	5.3	1802	2	US-09-586-106D-18	Sequence 18, Appl	957	62.5	5.2	628	2	US-09-107-532A-5288	Sequence 5288, Ap
885	63	5.3	1802	2	US-10-799-870-18	Sequence 18, Appl	958	62.5	5.2	669	2	US-09-342-647-18	Sequence 18, Appl
886	63	5.3	2985	2	US-10-259-275-40	Sequence 40, Appl	959	62.5	5.2	785	2	US-09-134-000C-6650	Sequence 6650, Ap
887	63	5.3	80	2	US-09-248-796A-26578	Sequence 26578, A	960	62.5	5.2	796	2	US-09-270-767-06617	Sequence 06617, A
888	62.5	5.2	136	1	US-08-477-451-31	Sequence 31, Appl	961	62.5	5.2	796	2	US-09-270-767-06617	Sequence 58533, A
889	62.5	5.2	140	2	US-09-270-767-40416	Sequence 40416, A	962	62.5	5.2	796	2	US-09-902-540-10957	Sequence 10957, A
890	62.5	5.2	140	2	US-09-270-767-55632	Sequence 55632, A	963	62.5	5.2	796	2	US-09-902-540-10957	Sequence 23462, A
891	62.5	5.2	161	2	US-09-413-814-15	Sequence 15, Appl	964	62.5	5.2	91	2	US-09-248-796A-23462	Sequence 23462, A
892	62.5	5.2	183	2	US-09-107-532A-7197	Sequence 7197, Ap	965	62.5	5.2	112	2	US-09-489-039A-11704	Sequence 11704, A
893	62.5	5.2	191	2	US-09-270-767-40648	Sequence 40648, A	966	62.5	5.2	129	2	US-09-673-898-10	Sequence 59183, A
894	62.5	5.2	191	2	US-09-270-767-55864	Sequence 55864, A	967	62.5	5.2	129	2	US-09-605-703B-1246	Sequence 1246, Ap
895	62.5	5.2	197	2	US-09-486-147-40	Sequence 40648, A	968	62.5	5.2	250	2	US-09-270-767-43784	Sequence 43784, A
896	62.5	5.2	200	2	US-09-270-767-36009	Sequence 36009, A	969	62.5	5.2	254	2	US-09-248-796A-22532	Sequence 22532, A
897	62.5	5.2	200	2	US-09-270-767-51226	Sequence 51226, A	970	62.5	5.2	272	2	US-09-903-456-76	Sequence 76, Appl
898	62.5	5.2	214	2	US-09-710-279-774	Sequence 774, App	971	62.5	5.2	272	2	US-09-903-456-80	Sequence 80, Appl
899	62.5	5.2	221	2	US-09-248-796A-15088	Sequence 15088, A	972	62.5	5.2	272	2	US-09-903-456-81	Sequence 81, Appl
900	62.5	5.2	252	2	US-09-270-767-45203	Sequence 45203, A	973	62.5	5.2	280	2	US-09-902-540-10330	Sequence 10330, A
901	62.5	5.2	255	2	US-09-991-181-287	Sequence 287, App	974	62.5	5.2	283	2	US-09-903-456-88	Sequence 88, Appl
902	62.5	5.2	255	2	US-09-990-444-287	Sequence 287, App	975	62.5	5.2	288	2	US-09-903-456-84	Sequence 84, Appl
903	62.5	5.2	255	2	US-09-997-333-287	Sequence 287, App	976	62.5	5.2	290	2	US-09-134-001C-4893	Sequence 4893, Ap

977	62	5.2	292	2	US-09-903-456-82	Sequence 82, Appl	1050	61.5	5.1	260	2	US-09-540-236-3812	Sequence 3812, Ap
978	62	5.2	295	2	US-09-903-456-86	Sequence 86, Appl	1051	61.5	5.1	269	2	US-09-489-039A-9180	Sequence 9180, Ap
979	62	5.2	305	2	US-09-270-767-44944	Sequence 44944, A	1052	61.5	5.1	271	2	US-09-077-675A-12	Sequence 12, Appl
980	62	5.2	317	2	US-09-489-039A-9602	Sequence 9602, Ap	1053	61.5	5.1	271	2	US-09-077-674-12	Sequence 12, Appl
981	62	5.2	333	1	US-07-667-276A-7	Sequence 7, Appl1	1054	61.5	5.1	288	2	US-09-134-000C-5520	Sequence 5520, Ap
982	62	5.2	336	2	US-09-543-681A-7161	Sequence 7161, Ap	1055	61.5	5.1	289	2	US-09-489-039A-12390	Sequence 12390, A
983	62	5.2	331	1	US-08-560-098A-46	Sequence 46, Appl	1056	61.5	5.1	297	2	US-09-328-352-5769	Sequence 5769, Ap
984	62	5.2	335	1	US-07-759-568-1	Sequence 1, Appl1	1057	61.5	5.1	302	2	US-09-077-675A-7	Sequence 2, Appl1
985	62	5.2	335	1	US-08-450-393A-8	Sequence 8, Appl1	1058	61.5	5.1	302	2	US-09-077-675A-2	Sequence 2, Appl1
986	62	5.2	335	1	US-08-390-000A-5	Sequence 5, Appl1	1059	61.5	5.1	302	2	US-09-077-674-7	Sequence 7, Appl1
987	62	5.2	335	1	US-08-446-669-8	Sequence 8, Appl1	1060	61.5	5.1	302	2	US-09-077-674-8	Sequence 8, Appl1
988	62	5.2	335	2	US-09-045-583-53	Sequence 53, Appl	1061	61.5	5.1	339	2	US-09-543-681A-6653	Sequence 6653, Ap
989	62	5.2	335	2	US-09-534-185-53	Sequence 53, Appl	1062	61.5	5.1	339	2	US-09-270-767-38347	Sequence 38347, A
990	62	5.2	335	2	US-09-625-573-8	Sequence 8, Appl1	1063	61.5	5.1	349	2	US-09-760-767-53564	Sequence 53564, A
991	62	5.2	355	4	PCT-US95-00476-8	Sequence 8, Appl1	1064	61.5	5.1	350	2	US-09-875-076-22	Sequence 22, Appl
992	62	5.2	360	1	US-08-202-056-7	Sequence 7, Appl1	1065	61.5	5.1	353	2	US-09-077-675A-3	Sequence 3, Appl1
993	62	5.2	360	1	US-08-597-236-11	Sequence 11, Appl	1066	61.5	5.1	353	2	US-09-077-674-3	Sequence 3, Appl1
994	62	5.2	360	1	US-08-746-682A-11	Sequence 11, Appl	1067	61.5	5.1	361	2	US-09-077-675A-8	Sequence 8, Appl1
995	62	5.2	360	1	US-09-409-778-4	Sequence 4, Appl1	1068	61.5	5.1	361	2	US-09-077-674-8	Sequence 8, Appl1
996	62	5.2	361	2	US-09-710-279-184	Sequence 184, App	1069	61.5	5.1	362	2	US-09-077-675A-13	Sequence 13, Appl
997	62	5.2	384	2	US-09-491-577-16	Sequence 16, Appl	1070	61.5	5.1	366	2	US-09-077-674-13	Sequence 13, Appl
998	62	5.2	384	2	US-09-252-991A-25633	Sequence 25633, A	1071	61.5	5.1	366	2	US-09-170-4960-88	Sequence 88, Appl
999	62	5.2	393	2	US-09-489-039A-7574	Sequence 7574, Ap	1072	61.5	5.1	366	2	US-09-743-7428-7	Sequence 7, Appl1
1000	62	5.2	407	2	US-09-949-016-11348	Sequence 11348, A	1073	61.5	5.1	366	2	US-09-762-661A-5	Sequence 5, Appl1
1001	62	5.2	409	2	US-09-583-110-3749	Sequence 3749, Ap	1074	61.5	5.1	366	2	US-09-762-661A-7	Sequence 7, Appl1
1002	62	5.2	412	2	US-09-134-001C-3949	Sequence 3949, App	1075	61.5	5.1	366	2	US-09-364-425A-45	Sequence 45, Appl1
1003	62	5.2	413	2	US-09-107-433-3687	Sequence 3687, Ap	1076	61.5	5.1	366	2	US-09-743-475-4	Sequence 4, Appl1
1004	62	5.2	414	2	US-09-198-452A-414	Sequence 414, App	1077	61.5	5.1	366	2	US-09-743-475-6	Sequence 6, Appl1
1005	62	5.2	414	2	US-09-438-185A-396	Sequence 396, App	1078	61.5	5.1	376	1	US-08-465-976A-3	Sequence 3, Appl1
1006	62	5.2	415	2	US-09-799-978-28	Sequence 28, Appl	1079	61.5	5.1	376	1	US-08-982-412-3	Sequence 3, Appl1
1007	62	5.2	417	2	US-09-710-279-950	Sequence 950, App	1080	61.5	5.1	376	2	US-09-107-403-3-3823	Sequence 3823, Ap
1008	62	5.2	432	2	US-09-605-703B-1244	Sequence 1244, Ap	1081	61.5	5.1	379	2	US-09-740-035-4	Sequence 4, Appl1
1009	62	5.2	447	2	US-09-388-089B-2	Sequence 2, Appl1	1082	61.5	5.1	391	1	US-07-921-178A-2	Sequence 2, Appl1
1010	62	5.2	473	1	US-08-597-236-13	Sequence 13, Appl	1083	61.5	5.1	391	1	US-08-103-445-5	Sequence 5, Appl1
1011	62	5.2	473	1	US-08-746-682A-13	Sequence 13, Appl	1084	61.5	5.1	391	1	US-08-461-690B-5	Sequence 5, Appl1
1012	62	5.2	475	2	US-09-368-089B-12	Sequence 12, Appl	1085	61.5	5.1	391	1	US-08-501-003A-16	Sequence 16, Appl
1013	62	5.2	489	1	US-08-589-893-14	Sequence 14, Appl	1086	61.5	5.1	391	1	US-09-475-252A-13	Sequence 13, Appl
1014	62	5.2	489	1	US-08-589-893-22	Sequence 22, Appl	1087	61.5	5.1	392	2	US-09-489-039A-8713	Sequence 8713, Ap
1015	62	5.2	489	1	US-08-589-893-24	Sequence 24, Appl	1088	61.5	5.1	397	2	US-09-491-577-32	Sequence 32, Appl1
1016	62	5.2	489	1	US-08-589-893-24	Sequence 24, Appl	1089	61.5	5.1	411	1	US-08-741-134-6	Sequence 6, Appl1
1017	62	5.2	489	1	US-09-020-991-14	Sequence 14, Appl	1090	61.5	5.1	415	1	US-08-110-286A-6	Sequence 6, Appl1
1018	62	5.2	489	1	US-09-020-991-22	Sequence 22, Appl	1091	61.5	5.1	415	2	US-08-981-189B-10	Sequence 10, Appl
1019	62	5.2	489	1	US-09-062-890-14	Sequence 14, Appl	1092	61.5	5.1	415	2	US-08-482-744-6	Sequence 6, Appl1
1020	62	5.2	489	1	US-09-062-890-22	Sequence 22, Appl	1093	61.5	5.1	415	2	US-09-580-734-6	Sequence 6, Appl1
1021	62	5.2	489	1	US-09-062-890-24	Sequence 24, Appl	1094	61.5	5.1	415	2	US-08-374-009-6	Sequence 6, Appl1
1022	62	5.2	489	1	US-09-062-890-24	Sequence 24, Appl	1095	61.5	5.1	415	2	US-09-191-724-6	Sequence 6, Appl1
1023	62	5.2	489	2	US-09-388-089B-11	Sequence 11, Appl	1096	61.5	5.1	415	2	US-09-799-978-16	Sequence 16, Appl
1024	62	5.2	499	2	US-09-673-898-6	Sequence 6, Appl1	1097	61.5	5.1	415	2	US-09-252-991A-26638	Sequence 26638, A
1025	62	5.2	550	2	US-09-533-427-14	Sequence 14, Appl	1098	61.5	5.1	418	2	US-09-543-681A-7634	Sequence 7634, Ap
1026	62	5.2	567	2	US-09-560-639-7	Sequence 7, Appl1	1099	61.5	5.1	418	2	US-09-322-501-2	Sequence 2, Appl1
1027	62	5.2	567	2	US-09-173-151A-24	Sequence 24, Appl	1100	61.5	5.1	427	2	US-09-252-991A-28897	Sequence 28897, A
1028	62	5.2	567	2	US-09-032-337-39	Sequence 39, Appl	1101	61.5	5.1	469	2	US-08-956-171B-5245	Sequence 5245, Ap
1029	62	5.2	580	2	US-10-104-047-2215	Sequence 3215, Ap	1102	61.5	5.1	469	2	US-08-781-986A-5245	Sequence 5245, Ap
1030	62	5.2	582	2	US-08-194-560-2	Sequence 2, Appl1	1103	61.5	5.1	499	1	US-08-899-514-2	Sequence 2, Appl1
1031	62	5.2	610	2	US-09-134-001C-4416	Sequence 4416, Ap	1104	61.5	5.1	497	1	US-08-995-670-6	Sequence 6, Appl1
1032	62	5.2	638	2	US-09-533-427-3	Sequence 3, Appl1	1105	61.5	5.1	497	1	US-08-633-485-6	Sequence 6, Appl1
1033	62	5.2	687	2	US-09-376-781-6	Sequence 6, Appl1	1106	61.5	5.1	506	2	US-09-857-896A-8	Sequence 8, Appl1
1034	62	5.2	706	2	US-10-104-047-2651	Sequence 2651, Ap	1107	61.5	5.1	510	2	US-09-134-001C-3368	Sequence 3368, Ap
1035	62	5.2	747	2	US-09-538-092-957	Sequence 957, App	1108	61.5	5.1	524	1	US-08-853-659A-35	Sequence 35, Appl
1036	62	5.2	775	2	US-09-949-016-10040	Sequence 10040, A	1109	61.5	5.1	524	1	US-08-298-426-4	Sequence 4, Appl
1037	62	5.2	800	2	US-09-305-640-2	Sequence 2, Appl1	1110	61.5	5.1	524	1	US-09-602-787A-534	Sequence 534, App
1038	62	5.2	1186	1	US-08-602-737-6	Sequence 6, Appl1	1111	61.5	5.1	615	2	US-09-602-787A-536	Sequence 536, App
1039	62	5.2	1186	2	US-09-001-982-6	Sequence 6, Appl1	1112	61.5	5.1	615	2	US-09-583-110-3110	Sequence 3110, Ap
1040	62	5.2	1186	2	US-09-668-650-6	Sequence 6, Appl1	1113	61.5	5.1	615	2	US-09-538-092-1125	Sequence 1125, Ap
1041	62	5.2	1267	2	US-09-543-681A-6130	Sequence 6130, Ap	1114	61.5	5.1	615	2	US-09-120-117A-31	Sequence 31, Appl
1042	62	5.2	1330	2	US-09-495-714C-6	Sequence 6, Appl1	1115	61.5	5.1	615	2	US-09-248-796A-18612	Sequence 18612, A
1043	61.5	5.1	163	2	US-09-949-016-8171	Sequence 8171, Ap	1116	61.5	5.1	766	1	US-09-949-016-6547	Sequence 6547, Ap
1044	61.5	5.1	170	2	US-08-600-430-4	Sequence 4, Appl1	1117	61.5	5.1	817	1	US-08-381-931B-2	Sequence 2, Appl1
1045	61.5	5.1	170	2	US-09-710-279-1164	Sequence 1164, Ap	1118	61.5	5.1	865	2	US-09-302-540-10416	Sequence 10416, A
1046	61.5	5.1	186	2	US-09-134-001C-4085	Sequence 4085, Ap	1119	61.5	5.1	865	2	US-09-489-039A-12127	Sequence 12127, A
1047	61.5	5.1	186	2	US-09-902-540-11995	Sequence 11995, A	1120	61.5	5.1	865	2	US-09-437-277-3	Sequence 3, Appl1
1048	61.5	5.1	235	2	US-08-812-586-16	Sequence 16, Appl	1121	61.5	5.1	1065	2	US-09-543-681A-7112	Sequence 7112, Ap
1049	61.5	5.1	235	2	US-09-535-832A-17	Sequence 17, Appl	1122	61.5	5.1	2232	2	US-09-077-674-25	Sequence 25, Appl

1123	61.5	5.1	2232	2	US-09-660-541-25	Sequence 25, Appl	1196	61	5.1	2864	2	US-08-469-260A-394	Sequence 394, App
1124	61.5	5.1	2247	2	US-09-091-219-2	Sequence 2, Appl1	1197	61	5.1	2864	2	US-08-488-446-394	Sequence 394, App
1125	61.5	5.1	2247	2	US-09-660-541-2	Sequence 2, Appl1	1198	61	5.1	2864	2	US-08-467-344A-394	Sequence 394, App
1126	61.5	5.1	3066	2	US-08-952-127-12	Sequence 12, Appl	1199	61	5.1	2864	2	US-08-424-550B-394	Sequence 394, App
1127	61	5.1	95	2	US-09-248-796A-21665	Sequence 21665, A	1200	61	5.1	3011	2	US-08-811-566-20	Sequence 20, Appl
1128	61	5.1	122	2	US-09-710-279-102	Sequence 102, App	1201	61	5.1	3011	2	US-09-014-416-1	Sequence 1, Appl1
1129	61	5.1	175	1	US-08-408-095-11	Sequence 11, Appl	1202	61	5.1	3011	2	US-10-104-756-20	Sequence 20, Appl
1130	61	5.1	188	2	US-09-198-452A-1206	Sequence 1106, App	1203	61	5.1	3011	2	US-10-104-966-1	Sequence 1, Appl1
1131	61	5.1	189	2	US-09-080-643-4	Sequence 4, Appl1	1204	61	5.1	3011	2	US-09-552-572-9	Sequence 9, Appl1
1132	61	5.1	200	2	US-09-710-279-394	Sequence 394, App	1205	61	5.1	3011	2	US-09-929-955-1	Sequence 1, Appl1
1133	61	5.1	200	2	US-09-710-279-1242	Sequence 1242, App	1206	61	5.1	3011	2	US-10-259-275-20	Sequence 20, Appl
1134	61	5.1	202	2	US-08-657-749D-17	Sequence 17, Appl	1207	61	5.1	3012	2	US-08-811-566-2	Sequence 2, Appl1
1135	61	5.1	206	2	US-09-134-001C-3929	Sequence 3929, App	1208	61	5.1	3012	2	US-09-034-756-2	Sequence 2, Appl1
1136	61	5.1	207	2	US-08-559-397A-13	Sequence 13, Appl	1209	60.5	5.1	73	2	US-09-543-681A-6595	Sequence 6595, App
1137	61	5.1	209	2	US-08-559-397A-11	Sequence 11, Appl	1210	60.5	5.1	107	2	US-09-107-532A-5805	Sequence 5805, App
1138	61	5.1	225	2	US-09-252-991A-30213	Sequence 30213, A	1211	60.5	5.1	116	2	US-09-270-767-36280	Sequence 36280, App
1139	61	5.1	230	2	US-09-134-001C-3744	Sequence 3744, App	1212	60.5	5.1	116	2	US-09-270-767-51497	Sequence 51497, A
1140	61	5.1	239	2	US-09-710-279-978	Sequence 978, App	1213	60.5	5.1	157	2	US-09-270-767-32124	Sequence 32124, A
1141	61	5.1	241	2	US-09-489-039A-8397	Sequence 8397, App	1214	60.5	5.1	157	2	US-09-270-767-47341	Sequence 47341, A
1142	61	5.1	256	1	US-08-236-618A-6	Sequence 6, Appl1	1215	60.5	5.1	157	2	US-09-270-767-58298	Sequence 58298, A
1143	61	5.1	256	1	US-09-150-864A-6	Sequence 6, Appl1	1216	60.5	5.1	159	6	5208144-32	Patent No. 5208144
1144	61	5.1	256	2	US-08-012-269A-2	Sequence 2, Appl1	1217	60.5	5.1	194	2	US-09-270-767-34926	Sequence 34926, A
1145	61	5.1	256	2	US-09-623-545A-3	Sequence 3, Appl1	1218	60.5	5.1	194	2	US-09-270-767-50143	Sequence 50143, A
1146	61	5.1	256	4	PCT-US96-03965-2	Sequence 2, Appl1	1219	60.5	5.1	195	2	US-09-612-404B-2	Sequence 2, Appl1
1147	61	5.1	261	2	US-09-134-001C-3485	Sequence 3485, App	1220	60.5	5.1	195	2	US-10-055-364-2	Sequence 2, Appl1
1148	61	5.1	265	2	US-09-107-532A-6716	Sequence 6716, App	1221	60.5	5.1	197	2	US-09-270-767-58832	Sequence 58832, A
1149	61	5.1	272	2	US-09-903-456-78	Sequence 78, Appl	1222	60.5	5.1	198	2	US-09-976-461-5	Sequence 5, Appl1
1150	61	5.1	272	2	US-09-583-110-3171	Sequence 1171, App	1223	60.5	5.1	199	2	US-08-478-316-33	Sequence 33, Appl
1151	61	5.1	279	2	US-09-107-433-3691	Sequence 3691, App	1224	60.5	5.1	199	2	US-09-019-793A-33	Sequence 33, Appl
1152	61	5.1	281	2	US-10-121-857-45	Sequence 45, Appl	1225	60.5	5.1	200	1	US-08-799-464A-9	Sequence 9, Appl1
1153	61	5.1	285	2	US-09-543-681A-7666	Sequence 7666, App	1226	60.5	5.1	200	4	US-09-601-326-33	Sequence 33, Appl
1154	61	5.1	296	2	US-09-540-226-2583	Sequence 2583, App	1227	60.5	5.1	200	4	PCT-US95-09927-9	Sequence 9, Appl1
1155	61	5.1	296	2	US-09-438-185A-545	Sequence 545, App	1228	60.5	5.1	207	2	US-08-811-519-18	Sequence 18, Appl
1156	61	5.1	302	2	US-08-311-731A-173	Sequence 173, App	1229	60.5	5.1	222	2	US-09-270-767-42973	Sequence 42973, A
1157	61	5.1	338	2	US-09-107-532A-6222	Sequence 6222, App	1230	60.5	5.1	240	1	US-08-114-555A-6	Sequence 6, Appl1
1158	61	5.1	345	2	US-09-107-532A-5817	Sequence 5817, App	1231	60.5	5.1	240	2	US-08-559-397A-12	Sequence 12, Appl
1159	61	5.1	345	2	US-09-489-039A-7417	Sequence 7417, App	1232	60.5	5.1	269	2	US-09-248-796A-22276	Sequence 2276, A
1160	61	5.1	355	2	US-08-833-752-8	Sequence 8, Appl1	1233	60.5	5.1	280	2	US-08-652-877-6	Sequence 6, Appl1
1161	61	5.1	355	2	US-09-938-719-8	Sequence 8, Appl1	1234	60.5	5.1	280	2	US-08-476-515A-6	Sequence 6, Appl1
1162	61	5.1	355	2	US-09-939-226B-8	Sequence 8, Appl1	1235	60.5	5.1	283	1	US-08-118-470-78	Sequence 78, Appl
1163	61	5.1	355	2	US-09-938-703B-8	Sequence 8, Appl1	1236	60.5	5.1	283	4	PCT-US93-08528-78	Sequence 78, Appl
1164	61	5.1	358	2	US-09-248-796A-19081	Sequence 19081, A	1237	60.5	5.1	285	2	US-10-162-012-37	Sequence 37, Appl
1165	61	5.1	363	2	US-08-688-988-30	Sequence 30, Appl	1238	60.5	5.1	296	2	US-09-540-336-2856	Sequence 2856, App
1166	61	5.1	400	2	US-09-328-352-5768	Sequence 5768, App	1239	60.5	5.1	300	2	US-09-393-634-17	Sequence 17, Appl
1167	61	5.1	440	2	US-09-489-039A-12132	Sequence 12132, A	1240	60.5	5.1	342	1	US-08-742-011-2	Sequence 2, Appl1
1168	61	5.1	445	2	US-09-799-978-34	Sequence 34, Appl	1241	60.5	5.1	342	2	US-09-275-384B-5	Sequence 5, Appl1
1169	61	5.1	481	2	US-09-248-796A-18663	Sequence 18663, A	1242	60.5	5.1	342	2	US-09-116-498-2	Sequence 2, Appl1
1170	61	5.1	488	2	US-09-248-796A-15101	Sequence 15101, A	1243	60.5	5.1	342	2	US-09-449-437A-2	Sequence 2, Appl1
1171	61	5.1	489	2	US-09-710-279-2632	Sequence 2632, App	1244	60.5	5.1	342	2	US-09-517-605-9	Sequence 9, Appl1
1172	61	5.1	500	2	US-09-134-000C-4886	Sequence 4886, App	1245	60.5	5.1	342	2	US-09-852-156-2	Sequence 2, Appl1
1173	61	5.1	503	2	US-09-134-001C-3948	Sequence 3948, App	1246	60.5	5.1	342	2	US-09-721-341-9	Sequence 9, Appl1
1174	61	5.1	545	2	US-09-949-016-6469	Sequence 6469, App	1247	60.5	5.1	342	2	US-09-721-495B-9	Sequence 9, Appl1
1175	61	5.1	558	2	US-09-949-016-7736	Sequence 7736, App	1248	60.5	5.1	349	2	US-09-710-479-932	Sequence 932, App
1176	61	5.1	672	2	US-09-556-916-26	Sequence 26, Appl	1249	60.5	5.1	352	2	US-09-489-039A-9155	Sequence 9155, App
1177	61	5.1	672	2	US-09-556-916-28	Sequence 28, Appl	1250	60.5	5.1	357	2	US-09-107-532A-5132	Sequence 5132, App
1178	61	5.1	718	2	US-09-487-558B-388	Sequence 388, App	1251	60.5	5.1	359	1	US-08-748-485-5	Sequence 5, Appl1
1179	61	5.1	724	2	US-09-252-991A-30228	Sequence 30228, A	1252	60.5	5.1	359	2	US-09-875-076-28	Sequence 28, Appl
1180	61	5.1	732	2	US-10-160-748-6	Sequence 6, Appl1	1253	60.5	5.1	388	2	US-09-252-991A-22979	Sequence 22979, A
1181	61	5.1	737	2	US-09-248-796A-14319	Sequence 14319, A	1254	60.5	5.1	397	2	US-09-107-532A-4918	Sequence 4918, App
1182	61	5.1	746	2	US-09-248-796A-17109	Sequence 17109, A	1255	60.5	5.1	409	1	US-08-743-130A-2	Sequence 2, Appl1
1183	61	5.1	774	2	US-10-104-047-2554	Sequence 17109, A	1256	60.5	5.1	409	1	US-08-743-130A-39	Sequence 39, Appl
1184	61	5.1	806	2	US-09-833-466-13	Sequence 2554, App	1257	60.5	5.1	417	2	US-09-248-796A-16410	Sequence 16410, A
1185	61	5.1	815	2	US-09-107-433-5059	Sequence 13, Appl	1258	60.5	5.1	421	2	US-10-104-047-3536	Sequence 3536, App
1186	61	5.1	848	2	US-09-583-110-2738	Sequence 5059, App	1259	60.5	5.1	424	2	US-09-161-994A-4	Sequence 4, Appl1
1187	61	5.1	915	2	US-09-538-092-577	Sequence 2738, App	1260	60.5	5.1	446	2	US-09-489-039A-9587	Sequence 9587, App
1188	61	5.1	980	2	US-09-107-532A-3714	Sequence 3714, App	1261	60.5	5.1	446	2	US-09-830-230A-90	Sequence 90, Appl
1189	61	5.1	985	2	US-09-949-016-8011	Sequence 8011, App	1262	60.5	5.1	451	2	US-09-328-352-5044	Sequence 5044, App
1190	61	5.1	1299	2	US-09-252-991A-31121	Sequence 31121, App	1263	60.5	5.1	473	2	US-09-604-231-2	Sequence 2, Appl1
1191	61	5.1	1336	2	US-09-949-016-9879	Sequence 9879, App	1264	60.5	5.1	473	2	US-09-489-039A-14199	Sequence 14199, A
1192	61	5.1	1503	2	US-09-600-087-2	Sequence 2, Appl1	1265	60.5	5.1	475	2	US-09-270-767-43745	Sequence 43745, A
1193	61	5.1	1503	2	US-09-949-016-6341	Sequence 6341, App	1266	60.5	5.1	482	2	US-09-830-230A-89	Sequence 89, Appl
1194	61	5.1	1529	2	US-09-949-016-11100	Sequence 11100, A	1267	60.5	5.1	487	2	US-09-724-224-8	Sequence 8, Appl1
1195	61	5.1	2079	2	US-09-949-016-8301	Sequence 8301, App	1268	60.5	5.1	487	2	US-10-093-317-8	Sequence 8, Appl1

1269	60.5	5.1	489	2	US-09-386-536-2	Sequence 2, Appl1	1342	60	5.0	330	2	US-09-543-681A-7116	Sequence 7116, Ap
1270	60.5	5.1	490	2	US-09-248-796A-19910	Sequence 19910, A	1343	60	5.0	333	2	US-09-170-496b-8	Sequence 8, Appl1
1271	60.5	5.1	490	2	US-09-949-016-8784	Sequence 8784, Ap	1344	60	5.0	333	2	US-09-170-496b-168	Sequence 168, Appl
1272	60.5	5.1	498	2	US-09-107-532A-5082	Sequence 5082, Ap	1345	60	5.0	333	2	US-09-826-509-509	Sequence 509, App
1273	60.5	5.1	498	2	US-09-583-110-2949	Sequence 2949, Ap	1346	60	5.0	341	2	US-09-802-540-11473	Sequence 11473, A
1274	60.5	5.1	499	2	US-09-710-879-1558	Sequence 1558, Ap	1347	60	5.0	347	2	US-09-107-532A-6019	Sequence 6019, Ap
1275	60.5	5.1	503	2	US-09-068-195-24	Sequence 24, Appl	1348	60	5.0	359	2	US-09-107-532A-6455	Sequence 6455, Ap
1276	60.5	5.1	510	2	US-09-107-433-2618	Sequence 2618, Ap	1349	60	5.0	360	2	US-09-270-767-32827	Sequence 32827, A
1277	60.5	5.1	512	2	US-09-124-224-4	Sequence 4, Appl1	1350	60	5.0	360	2	US-09-270-767-48044	Sequence 48044, A
1278	60.5	5.1	512	2	US-10-093-317-4	Sequence 4, Appl1	1351	60	5.0	376	2	US-09-107-532A-6448	Sequence 6448, Ap
1279	60.5	5.1	519	2	US-09-248-796A-20852	Sequence 20852, A	1352	60	5.0	377	2	US-09-316-080-5	Sequence 5, Appl1
1280	60.5	5.1	533	2	US-09-489-039A-7452	Sequence 7452, Ap	1353	60	5.0	377	2	US-09-110-760-5	Sequence 5, Appl1
1281	60.5	5.1	536	2	US-09-107-532A-5507	Sequence 5507, Ap	1354	60	5.0	382	2	US-09-134-001C-4483	Sequence 4483, Ap
1282	60.5	5.1	537	2	US-09-134-001C-4091	Sequence 4091, Ap	1355	60	5.0	387	1	US-08-902-853-6	Sequence 6, Appl1
1283	60.5	5.1	554	2	US-09-134-001C-5109	Sequence 5109, Ap	1356	60	5.0	397	1	US-08-990-379-8	Sequence 8, Appl1
1284	60.5	5.1	554	2	US-09-543-681A-5774	Sequence 5774, Ap	1357	60	5.0	416	2	US-09-583-110-2712	Sequence 2732, Ap
1285	60.5	5.1	558	2	US-09-540-236-2943	Sequence 2943, Ap	1358	60	5.0	416	2	US-10-140-372-4	Sequence 4, Appl1
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## ALIGNMENTS

RESULT 1  
US-10-104-047-2567  
; Sequence 2567, Application US/10104047  
; GENERAL INFORMATION:  
; PATENT No. 6943241  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. 6943241el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2567  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-2567  
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Best Local Similarity 87.5%; Pred. No. 3.9e-69;  
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DB 121 RHMWIAIAVSMCMGSG-SPPVLVAKSCQAM 151  
RESULT 2  
US-08-691-814B-6  
; Sequence 6, Application US/08691814B  
; Patent No. 5981218  
; GENERAL INFORMATION:  
; APPLICANT: Rio, Marie-Christine  
; APPLICANT: Tomasetto, Catherine  
; APPLICANT: Bassett, Paul  
; APPLICANT: Byrne, Jennifer  
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful  
; TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis  
; NUMBER OF SEQUENCES: 124  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Ave, NW, Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA

ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/691,814B  
FILING DATE: 31-Jul-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/002,183  
FILING DATE: 09-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K. 668  
REGISTRATION NUMBER: 36,668  
REFERENCE/DOCKET NUMBER: 1383.0090001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-691-814B-6

Query Match 55.6%; Score 664; DB 1; Length 445;  
Best Local Similarity 56.2%; Pred. No. 6.3e-68;  
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RESULT 3  
US-09-949-016-8594  
Sequence 8594, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8594  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8594

Query Match 7.2%; Score 85.5; DB 2; Length 449;  
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DB 392 EGLGGAAYVNT---FHNIALETSDHR 416

RESULT 4  
US-08-846-762-92  
Sequence 92, Application US/08846762A  
Patent No. 5994072

GENERAL INFORMATION:  
APPLICANT: Lam, Joseph S.  
APPLICANT: Burrows, Lori  
APPLICANT: Charter, Deborah  
APPLICANT: de Kievit, Teresa  
TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly  
FILE REFERENCE: 6580-089  
CURRENT APPLICATION NUMBER: US/08/846,762A  
CURRENT FILING DATE: 1997-04-30  
NUMBER OF SEQ ID NOS: 100  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 92

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DB 1 TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-08-846-762-92

Query Match 6.9%; Score 82.5; DB 1; Length 341;  
Best Local Similarity 24.0%; Pred. No. 0.67;  
Matches 31; Conservative 20; Mismatches 51; Indels 27; Gaps 4;

QY 47 GISDVARTFCLFVTFDLLFVTLMIETLVNNGIENLTLEKEVMQDYSSYDFILFVAVFRK 106  
DB 233 GWIDTRFFFCWILLLGLFYVDATWTLVRYLGSKF-----VYAHRSHG--YQIASR 282  
QY 107 RPKVILAVVCRRLHWMALITTAVTSAFLAKVILSKLFSQAGFVLPITISITLMIETWFL 166  
DB 283 RPK-----RLPVTLSAIAINIMLFPALLAGL-----NIVNPITAIITISYI 325

QY 167 ETWFLDFKVL 175  
DB 326 PLVYIDYKL 334

RESULT 5  
US-09-489-0394-9711  
Sequence 9711, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 9711  
LENGTH: 350

TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-9711

Query Match  
Best Local Similarity 31.8%; Pred. No. 1.2;  
Matches 21; Conservative 15; Mismatches 21; Indels 9; Gaps 3;

QY 111 LILAAVACRLHMMWALTTAVTSAPFLAKVILSKL-----FSQGAFCGYVLPISF---IL 163  
DB 83 LLLAAVSLPLAPMMWVVLGTRF--AVVIAQLYGLGHNPENPMIGVYVLLISFPQMT 140

QY 164 AMIETW 169  
DB 141 SWLPSY 146

RESULT 6  
US-10-226-629A-16  
Sequence 16, Application US/10226629A  
Patent No. 6960431  
GENERAL INFORMATION:  
APPLICANT: Myriad Genetics, Inc.  
APPLICANT: Morham, Scott  
APPLICANT: Zavit, Kenton  
APPLICANT: Hobden, Adrian  
TITLE OF INVENTION: Therapeutic Compositions and Methods for Treating Viral Infection  
FILE REFERENCE: 5006.01  
CURRENT APPLICATION NUMBER: US/10/226,629A  
CURRENT FILING DATE: 2002-08-22  
PRIOR APPLICATION NUMBER: US 60/314,182  
PRIOR FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 736  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 16  
LENGTH: 891  
TYPE: PRT  
ORGANISM: Vaccinia virus  
US-10-226-629A-16

Query Match  
Best Local Similarity 23.3%; Pred. No. 4.5;  
Matches 38; Conservative 36; Mismatches 70; Indels 19; Gaps 7;

QY 7 DMENALTGSSSHSLRNHISINPTOLMAR-IESYEGREKKGISDVRTFCLFVTFDLIF 65  
DB 717 NMTBEIT--DWINSLSKTKTISKNNMLVSGALNSVANSKQKIGDLRQSSCKMALLPKUL 774  
QY 66 VTLIMITELNNGIENTLEKEVNO-YDY-----SIFDIFLLAVFRFKVLLIAYVCR 119  
DB 775 ATSIYTERIFNAKGDVAKSMLEKYVFTDISMSLYKDLIAMENLKMLYIIRSGCR 834  
QY 120 LRHMMALALT--AVTSAPFLAKVILSKL-----FSQGAFCGYV 155  
DB 835 IDD---AQITTDLVKYSILIRPKILSMNTYNNEMSKRGYFEHM 874

RESULT 7  
US-09-171-699-4  
Sequence 4, Application US/09171699  
Patent No. 6448389  
GENERAL INFORMATION:  
APPLICANT: The Wistar Institute of, Anatomy & Biology  
Berencsi, Klara  
Kari, Csaba  
TITLE OF INVENTION: No. 6448389el Cytomegalovirus DNA Constructs and  
Uses Therefor  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Howson and Howson  
STREET: Spring House Corporate Center, P.O. Box 457  
CITY: Spring House

STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/171,699  
FILING DATE: 19-Jan-1999  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/015,717  
FILING DATE: 23-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Kodloff, Cathy A.  
REGISTRATION NUMBER: 33,980  
REFERENCE/DOCKET NUMBER: MST66APCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-171-699-4  
Query Match  
Best Local Similarity 19.3%; Pred. No. 1.9;  
Matches 52; Conservative 36; Mismatches 67; Indels 115; Gaps 12;

QY 14 GSQSHSLRNHISINPTOLMARIESY-----EGREKKGISDVRTFCLFVTFDLIFVTL 68  
DB 142 GCSQSHSLRNHISINPTOLMARIESY-----EGREKKGISDVRTFCLFVTFDLIFVTL 190  
QY 69 LMIIEELNNGIENTLEKEVNOYDY-----YSSYFDIFLLAVFRFKVLLIAYVCR 120  
DB 191 L-----TTCVETMCNEKYVTSACMTWVGISLSEF-----CRV 226  
QY 121 RHMMAITTAVTSAPFLAK-----VLSKLFSGAGGYL----- 156  
DB 227 LSCVLEETSV-----MLARPLITKEVISVKKRIEICMKVFAQ-----YILGADPLR 277  
QY 157 ---PIISFILAMIEFWLDFKVLPOEAEEFNRLIVODASERAAALIPGSLSDGQFYSPP 213  
DB 278 VCSBSVD-----DLRAIAESDEBEALVATLATR-----GASSSDSVSPPE 320  
QY 214 S-----EAGSEAEKODSEK 229  
DB 321 SPVPATIPLSSVIAENSDDSESDSEK 350

RESULT 8  
PCT-US94-02107-2  
Sequence 2, Application PC/TUS9402107  
GENERAL INFORMATION:  
APPLICANT: The Wistar Institute of, Anatomy and Biology  
TITLE OF INVENTION: Recombinant Cytomegalovirus Vaccine  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr, PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/02107  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/017,130  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST6BPCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-02107-2

Query Match 6.7%; Score 79.5; DB 4; Length 406;  
Best Local Similarity 19.3%; Pred. No. 1.9;  
Matches 52; Conservative 36; Mismatches 67; Indels 115; Gaps 12;

QY 14 GSSSHASLNHISINTQLMARIESY-----EGREKKISDVARTCLFVTFPLLVTL 68  
DB 142 GCSQAMALONLPCQSPDEIMAYOKIFKILDEBRDK-----VLTHDHFMDI 190  
QY 69 LMIIELVNGIENTLEKEVMQVY-----YSSYEDFLAVFRFKVLLAVAVCR 120  
DB 191 L-----TCVETWCNEYKVTSDACMMTMGSLSEF-----CRV 226  
QY 121 RHWMALTTAVTSAPFLAK-----VLSKLFSGAGGVVL----- 156  
DB 227 LSCVLEETSV-----MLAKRPILTKREVISMKRRIEIMCKVFAQ-----YILGADPLR 277  
QY 157 ---PIISFILAMETWFLDFKVLPOBAEENRLLIVODASERALLFGSLSDGQFYSPPE 213  
DB 278 VCSFSVD-----DLRAIAESDEEAIIVAYTLATR-----GASSSDSLVSPPE 320  
QY 214 S-----EAGSEAEKODSEK 229  
DB 321 SPVPATPLSSVIVAENSDEESQSDPEE 350

## RESULT 9

US-09-976-594-503  
Sequence 503 Application US/09976594  
Patent No. 6673549  
GENERAL INFORMATION:  
APPLICANT: Furness, Michael  
APPLICANT: Buchbinder, Jenny  
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
FILE REFERENCE: PA-0041 US  
CURRENT APPLICATION NUMBER: US/09/976,594  
CURRENT FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/240,409  
PRIOR FILING DATE: 2000-10-12  
NUMBER OF SEQ ID NOS: 1143  
SOFTWARE: PERL Program  
SEQ ID NO 503  
LENGTH: 723  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6673549 2246292CD1  
US-09-976-594-503

Query Match 6.7%; Score 79.5; DB 2; Length 723;  
Best Local Similarity 18.0%; Pred. No. 4.3;  
Matches 34; Conservative 40; Mismatches 58; Indels 57; Gaps 8;

QY 58 FVTFDLFVTLMIETLVNNGIENTLEKEVMQVYSSYEDFLAVFRFKVLI----- 112  
DB 13 FMSVDICVTAIVF-----SHLDRSLIEDIRFNFDSVLDIMACLVRSCLLGATIG 67  
QY 113 ----LAVAVCRIR-HMMAIALTTAVTSAPFLAKVILSKLFSQ-----GAFGY 154  
DB 68 VAKNSALGPRRLASNLVLSVLCFVGITAMVKLL--LFSEVRRIIDPMFWALFVWY 124  
QY 155 VLPISFILAMETWFLDFKVLPOBAEENRLLIVODASERALLFGSLSDGQFY----- 209  
DB 125 ISLGASFLMWL-----LSTVRPGIQ--ALPBGATIEAGFPGSGR 163  
QY 210 SPSEENGS 218  
DB 164 PPEQASGA 172

## RESULT 10

US-09-270-767-41033  
Sequence 41033 Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 41033  
LENGTH: 221  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-41033

Query Match 6.6%; Score 78.5; DB 2; Length 221;  
Best Local Similarity 22.5%; Pred. No. 1.1;  
Matches 38; Conservative 33; Mismatches 73; Indels 25; Gaps 7;

QY 56 CLFVTFDL--LFTVLMIIETLVNNGIENTLEKEVMQVYSSYEDFLAVFRFKVLI 112  
DB 17 CIYVSSMDQFLFIILILILITCLSFVEKYLFTVNILXIDNYIGKXNVFLFLLFOXII 76  
QY 113 LAVAVCRIR-HMMAIALTT--AVTSAPFLAKVILSKLFSOGAGGVVL--PIISFILAMETW 169  
DB 77 VVVFCSFCCTYGLIGQTVNSINFRNLKXLSLT-----LGLFLSPISIHFSVLPXY 129  
QY 170 FLDFKVLPOBAEENRLL-----IVODASERALL--IPGLSLDQGF 208  
DB 130 LVNNSVTLKXVXIOEFLDXVVCFFFIILASPRFLCKIIPNGL--GQF 176

## RESULT 11

US-09-270-767-56249  
Sequence 56249 Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 56249  
LENGTH: 221  
TYPE: PRT



```

; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56249

```

Query Match	6.6%	Score 78.5	DB 2	Length 221
Best Local Similarity	22.5%	Pred. No. 1.1		
Matches 38	Conservative 33	Mismatches 73	Indels 25	Gaps 7

[illegible]

```

QY      170 FLDFKVLPEAEENRLL-----IVQDASEAAL--IPGLSDGF 208
      :: || : | | | | | | | | | |
DB      130 LVNNSVHLKNVXIQLFDLVVKCFPILRASFRCCLKDIPNGL--GQF 176

```

```

RESULT 12
US-09-724-653-2
; Sequence 2, Application US/09724653
; Patent No. 6830913
; GENERAL INFORMATION:
; APPLICANT: Lin9, Victor
; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: APT-004CP
; CURRENT APPLICATION NUMBER: US/09/724,653
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 766
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-724-653-2

```

Query Match	6.6%;	Score 78.5;	DB 2;	Length 766;
Best Local Similarity	18.0%;	Pred. No. 6.1;		
Matches	34;	Conservative	39;	Mismatches 59;
				Indels 57;
				Gaps 8

```

QY 58 PFTPLDLFLTLMIIEILNNGGIENTLEKRVQDYXSSYEDFJFLAYPEFKUL----- 112
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 13 FMSVDICVTTAYVFP-----SHIDRSLEDIRHFNFIDSVLDLMAACTVRSCLLIGATTG 67
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 113 ---LAVAVCRDR-HWMAIALTTAVASAFLLAKVILSKLFSQ-----GAGFY 154
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 68 VAKNSALGGRRLRASLVLTIVCLFPGIYAMVTL---LFSEVRRIPIRDPWFALFVWTY 124
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 155 VLPITISFIITAMETWFLDFKVLPOEAEENRLLIYODASERALLPGGLSDGQFY----- 209
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 125 ISLGASFLLMWL-----LSTVPRGTG--ALEPGAAATEARGFPQSGR 163
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 210 SPPESEAGS 218
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 164 PPPEQASGA 172
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 13  
 US-09-724-653-14  
 ; Sequence 14, Application US/09724653  
 ; Patent No. 6830913  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ling, Victor  
 ; TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF  
 ; FILE REFERENCE: AP2-004CP  
 ; CURRENT APPLICATION NUMBER: US/09/724,653  
 ; CURRENT FILING DATE: 2000-11-28

```

; PRIOR APPLICATION NUMBER: 60/167,930
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 14

```

ORGANISM: Homo sapiens  
US-09-724-653-14

Query Match	6.6%;	Score 78.5;	DB 2;	Length 766;
Best Local Similarity	18.0%;	Pred. No. 6.1;		
Matches	34;	Conservative	39;	Mismatches 59;
				Indels 57;
				Gaps 8

```

QY      FVTFDELLPFTLLMIITIELNANGGIEKTEKEMQDYSSSYDIFLILAVFFKKVL-----112
Db      FMSVDICVTTAIYVF-----SHLDRLSLEDIRHNFIEPDSVLDIMAACTLRSCLLLGATIG 67
QY      113 -----LAVNQCRR-HMMALTLTNTVTSAPLAKYLSLKFSQ-----GAFGY 154
Db      68 VAKNSLGRPRRLPASHVLTVCLEFVGYYAMKLL--LPSGVARRPIRDPWFNALLPWY 124

```

```

Oy      155 VLEPIIFIIAMIEITWFLDKVLPQAEENBNLLIYOASERFALIPGLSDGQY-----209
           |||::|
Db      125 ISGAGFLLMWL-----LSTVRPTQ-ALEPGATAEAGFPQSGR 163
           |||::|
Oy      210 SPPESEAGS 218
           |||::|
Db      164 PPPEQASGA 172

```

```

RESULT 14
US-09-724-653-15
: Sequence 15, Application US/09724653
: Patent No. 6830913
: GENERAL INFORMATION:
: APPLICANT: Ling, Victor
: TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
: FILE REFERENCE: AEP-004CP
: CURRENT APPLICATION NUMBER: US/09/724,653
: CURRENT FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: 60/167,930
: PRIOR FILING DATE: 1999-11-29
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 15
: LENGTH: 766
: TYPE: prt
: ORGANISM: Homo sapiens
US-09-724-653-15

```

Query Match	6.6%	Score 78.5	DB 2	Length 766
Best Local Similarity	18.0%	Pred. No. 6.1		
Matches 34	Conservative 39	Mismatches 59	Indels 57	Gaps 8

```

OY      58 FYVFDLLFVTLWIIELANNGGENTLEKXWQYYSYDFIDFLAVFRKVI----- 112
Db      13 FMSVDITVTAIVF-----SHDSSLEDIEDIHFNIFPSVDLMAACLYRSCLLGATIG 67

OY      113 ----LAVAVCRLE-HWMAIALTTAATVTSAPFLAKVILSKLFSQ-----GAFGY 15
Db      68 VAKNSALGPRRLPASPVLVITIVCLFVGIYAMVKLL--LFSEVRRPIRNDPMFALFWTY 124

OY      155 VLPISFILAMIEITWFLDFKRVLPQEAEBENRLLIYQDSERALLPGSLSGOY----- 205
Db      125 ISLCASFLMLWML-----LSTVRPGTO--ALEPGATAEAGFPQSGR 163

OY      210 SPPESEAGS 218
Db      164 PPPEQASGA 172

```

## RESULT 15

```
US-09-248-796A-20444
; Sequence 20444, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Kelch Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ. ID NOS: 28208
; SEQ. ID NO 20444
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20444

Query Match      6.5%; Score 78; DB 2; Length 228;
Best Local Similarity 22.1%; Pred. No. 1.3;
Matches 32; Conservative 32; Mismatches 49; Indels 32; Gaps 7;

QY 63 LFPVTL-----LWIELNVN---GIENTLEKEVMQDYYSYF-----DIFLAVF 106
DB 91 LVFTALTSGAFWLSFPAINIPFTFGILAAVQKMTQSSALAPYLIMAILSFIMLLTF 150
QY 107 RFRVLLIYAVGCRRLRHWMALALTVAVTSAFLAKVILSKLSQAGFYVLPITISF----- 161
DB 151 KSTVLSGFLC-----LTALFSLLSASYVGSVALTK--AAGAFGVIAVVAALYDTFA 202
QY 162 ILAMIETWFLDFKVLDP---QEAEDEE 183
DB 203 LIATKQNSYPTLPVLPPLGSEAKQE 227
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Search completed: May 12, 2006, 20:48:56  
Job time : 61 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2006, 21:12:04 ; Search time 66 Seconds  
(without alignments)  
1481.395 Million cell updates/sec

Perfect score: 1195  
Sequence: 1 MNHLPEDMENALTGSSQSSHA.....EAGSEPAEKQDSKPLLEL 234

Scoring table: BLOSUM62  
Gap10.0 , Gapect 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : Published Applications\_AA\_Main.\*  
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4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
449	1195	100.0	234	4	US-10-223-085-62 Sequence 62, Appl
466	1195	100.0	234	4	US-10-223-084-62 Sequence 62, Appl
467	1195	100.0	234	4	US-10-223-088-62 Sequence 62, Appl
468	1195	100.0	234	4	US-10-223-090-62 Sequence 62, Appl
470	1195	100.0	234	4	US-10-223-087-62 Sequence 62, Appl
478	1195	100.0	234	4	US-10-223-083-62 Sequence 62, Appl
481	1195	100.0	234	4	US-10-223-089-62 Sequence 62, Appl
488	1195	100.0	234	4	US-10-174-587-66 Sequence 66, Appl
522	1195	100.0	234	4	US-10-063-742-14 Sequence 62, Appl
560	1195	100.0	234	4	US-10-223-081-62 Sequence 62, Appl
650	1195	100.0	234	4	US-10-223-082-62 Sequence 62, Appl
665	1195	100.0	234	4	US-10-144-194A-20 Sequence 20, Appl
670	1195	100.0	234	4	US-10-305-654-62 Sequence 62, Appl
675	1195	100.0	234	4	US-10-081-056-62 Sequence 62, Appl
681	1195	100.0	234	5	US-10-491-556-20 Sequence 20, Appl
682	1195	100.0	234	5	US-10-972-317-14 Sequence 14, Appl
683	1195	100.0	234	5	US-10-485-555-36 Sequence 36, Appl
687	1188	99.4	234	4	US-10-262-839-84 Sequence 84, Appl
688	1024	89.7	201	4	US-10-264-237-2663 Sequence 2663, Ap
689	985	82.4	198	4	US-10-262-839-82 Sequence 82, Appl
690	669.5	56.0	176	4	US-10-104-047-2567 Sequence 2567, Ap
691	664	55.6	145	4	US-10-177-293-236 Sequence 296, App
692	664	55.6	445	4	US-10-435-696-33 Sequence 33, Appl
693	625	52.3	534	5	US-10-450-763-35857 Sequence 35857, A
694	578	48.4	412	5	US-10-491-213-22 Sequence 22, Appl
695	343	28.7	580	6	US-11-097-143-6696 Sequence 6696, Ap
696	91	7.6	373	4	US-10-091-007-198 Sequence 198, App
697	90.5	7.6	803	4	US-10-437-963-136814 Sequence 136814,

698	87.5	7.3	516	3	US-09-925-298-653 Sequence 653, App
699	87.5	7.3	516	4	US-10-102-806-653 Sequence 653, App
700	87	7.3	421	5	US-10-741-600-922 Sequence 929, App
701	85.5	7.2	223	5	US-10-741-600-926 Sequence 926, App
702	85.5	7.2	285	5	US-10-741-600-921 Sequence 921, App
703	85.5	7.2	315	5	US-10-741-600-925 Sequence 925, App
704	85.5	7.2	323	5	US-10-741-600-923 Sequence 923, App
705	85.5	7.2	328	5	US-10-741-600-924 Sequence 924, App
706	85.5	7.2	338	5	US-10-741-600-928 Sequence 928, App
707	85.5	7.2	339	5	US-10-741-600-930 Sequence 930, App
708	85.5	7.2	384	5	US-10-741-600-932 Sequence 932, App
709	85.5	7.2	390	5	US-10-741-600-927 Sequence 927, App
710	85.5	7.2	396	4	US-10-282-122A-54604 Sequence 54604, A
711	85.5	7.2	438	5	US-10-741-600-931 Sequence 931, App
712	85.5	7.2	440	4	US-10-262-511-182 Sequence 182, App
713	85.5	7.2	473	4	US-10-264-237-2016 Sequence 2016, App
714	85.5	7.2	473	5	US-10-723-860-872 Sequence 872, App
715	85.5	7.2	500	4	US-10-282-122A-68468 Sequence 68468, A
716	85	7.1	500	4	US-10-425-115-334089 Sequence 334089, Sequence 65247, A
717	85	7.1	527	4	US-10-425-114-65347 Sequence 11433, A
718	85	7.1	797	5	US-10-156-761-11433 Sequence 22362, A
719	85	7.1	797	5	US-10-732-923-22362 Sequence 332914, A
720	84.5	7.1	102	4	US-10-425-115-332914 Sequence 61134, A
721	84.5	7.1	430	4	US-10-282-122A-61134 Sequence 111543, A
722	84.5	7.1	886	4	US-10-437-963-111543 Sequence 51644, A
723	83.5	7.0	422	5	US-10-450-763-51644 Sequence 61960, A
724	82.5	6.9	239	4	US-10-282-122A-65332 Sequence 92, Appl
725	82.5	6.9	341	4	US-10-216-409-92 Sequence 126, App
726	82.5	6.9	399	5	US-10-831-070-126 Sequence 144, App
727	82	6.9	589	4	US-10-205-194-144 Sequence 1543, App
728	82	6.9	1466	5	US-10-732-923-1543 Sequence 4166, A
729	81.5	6.8	264	4	US-10-425-114-4166 Sequence 272132, A
730	81.5	6.8	436	4	US-10-424-999-272132 Sequence 12846, A
731	81.5	6.8	659	4	US-10-437-963-128426 Sequence 223855, A
732	81	6.8	525	4	US-10-425-115-253855 Sequence 5808, App
733	81	6.8	529	4	US-10-369-493-5808 Sequence 5809, App
734	81	6.8	463	4	US-10-369-493-5809 Sequence 60960, A
735	80.5	6.7	463	4	US-10-282-122A-60960 Sequence 15, App
736	80.5	6.7	536	5	US-10-498-327-165 Sequence 16, Appl
737	80.5	6.7	891	4	US-10-226-629A-16 Sequence 851, App
738	80	6.7	144	3	US-09-925-497-851 Sequence 258202, A
739	80	6.7	209	4	US-10-425-115-258202 Sequence 3158, App
740	80	6.7	238	4	US-10-108-460A-3158 Sequence 1308, App
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747	79.5	6.7	558	4	US-10-425-115-114242 Sequence 4, Appl1
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751	79	6.6	210	4	US-10-425-115-258203 Sequence 8178, App
752	79	6.6	264	4	US-10-425-115-258201 Sequence 110, App
753	79	6.6	323	5	US-10-732-923-18557 Sequence 29323, A
754	79	6.6	1531	6	US-10-353-690-1110 Sequence 4244, App
755	79	6.6	1597	3	US-09-832-292-35 Sequence 17, Appl
756	79	6.6	135	4	US-10-029-386-29323 Sequence 14, Appl
757	78.5	6.6	228	5	US-10-501-382-4244 Sequence 17, Appl
758	78.5	6.6	766	4	US-10-072-621-6 Sequence 6, Appl1
759	78.5	6.6	766	4	US-10-156-239-17 Sequence 17, Appl
760	78.5	6.6	766	4	US-10-199-485-17 Sequence 1, Appl
761	78.5	6.6	766	4	US-10-343-903-14 Sequence 2, Appl1
762	78.5	6.6	766	5	US-10-802-513-14 Sequence 14, Appl
763	78.5	6.6	766	5	US-10-802-513-14 Sequence 19, Appl
764	78.5	6.6	766	5	US-10-802-513-15 Sequence 9, Appl1
765	78.5	6.6	766	5	US-09-938-719-9 Sequence 9, Appl1
766	78.5	6.6	355	3	US-09-939-226-9 Sequence 9, Appl1
767	78	6.5	355	3	US-09-938-703-9 Sequence 9, Appl1
768	78	6.5	355	3	US-09-938-703-9 Sequence 9, Appl1
769	78	6.5	355	3	US-09-938-703-9 Sequence 9, Appl1
770	78	6.5	355	3	US-09-938-703-9 Sequence 9, Appl1

771	78	6.5	355	4	US-10-661-798-9	Sequence 9, Appl1	844	74.5	6.2	471	3	US-09-929-313-4	Sequence 4, Appl1
772	78	6.5	355	4	US-10-612-791-9	Sequence 9, Appl1	845	74.5	6.2	500	4	US-10-767-701-41924	Sequence 41924, A
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775	77.5	6.5	280	4	US-10-243-552-905	Sequence 905, App	848	74.5	6.2	1550	5	US-10-732-923-1682	Sequence 1682, Ap
776	77.5	6.5	280	5	US-10-450-763-47733	Sequence 47733, A	849	74.5	6.2	3010	4	US-10-333-442A-34	Sequence 34, Appl
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778	77.5	6.5	337	4	US-10-437-963-163107	Sequence 163107, A	851	74	6.2	301	4	US-10-424-599-26067	Sequence 26067, A
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781	77.5	6.5	892	4	US-10-226-629A-15	Sequence 15, Appl	854	74	6.2	332	5	US-10-617-320-2682	Sequence 2682, Ap
782	77.5	6.5	1476	5	US-10-732-923-1679	Sequence 1679, Ap	855	74	6.2	342	4	US-10-243-552-467	Sequence 467, App
783	77	6.4	650	4	US-10-282-122A-44096	Sequence 44096, A	856	74	6.2	350	4	US-10-112-356-7	Sequence 7, Appl
784	77	6.4	735	4	US-10-437-963-162148	Sequence 162148, A	857	74	6.2	485	4	US-10-424-599-260883	Sequence 164, App
785	77	6.4	1391	4	US-10-437-963-128935	Sequence 128935, A	858	74	6.2	485	4	US-10-369-493-6580	Sequence 6580, Ap
786	76.5	6.4	135	5	US-10-739-930-69321	Sequence 6932, Ap	859	74	6.2	491	4	US-10-859-149-11	Sequence 11, Appl
787	76.5	6.4	453	4	US-10-437-963-156098	Sequence 156098, A	860	74	6.2	629	4	US-10-424-599-247076	Sequence 247076, A
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791	76.5	6.4	570	4	US-10-415-187-3	Sequence 3, Appl1	864	73.5	6.2	253	4	US-10-424-599-260883	Sequence 260883, A
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793	76.5	6.4	593	4	US-10-335-977-6023	Sequence 6023, Ap	866	73.5	6.2	291	4	US-10-437-963-164729	Sequence 164729, A
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796	76.5	6.4	2539	4	US-10-369-493-3779	Sequence 3779, Ap	869	73.5	6.2	491	4	US-10-203-915A-1	Sequence 1, Appl1
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798	76	6.4	456	4	US-10-264-237-1800	Sequence 1800, Ap	871	73.5	6.2	491	4	US-10-335-977-8879	Sequence 8879, Ap
799	76	6.4	557	3	US-09-925-399-940	Sequence 940, App	872	73.5	6.2	574	4	US-10-972-024-247	Sequence 247, App
800	76	6.4	557	3	US-09-925-399-940	Sequence 940, App	873	73.5	6.2	577	5	US-10-369-493-17311	Sequence 17311, A
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802	76	6.4	1551	5	US-10-732-923-1738	Sequence 1738, Ap	875	73.5	6.2	1287	5	US-11-097-143-12003	Sequence 12003, A
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805	75.5	6.3	228	6	US-11-097-143-16242	Sequence 16242, A	878	73	6.1	114	4	US-10-335-977-8879	Sequence 8879, Ap
806	75.5	6.3	253	4	US-10-437-963-188833	Sequence 188833, A	879	73	6.1	114	4	US-09-828-644-114	Sequence 114, App
807	75.5	6.3	263	3	US-09-769-787-119	Sequence 119, App	880	73	6.1	189	3	US-10-335-977-5926	Sequence 5926, Ap
808	75.5	6.3	264	5	US-10-617-320-4877	Sequence 4877, Ap	881	73	6.1	265	4	US-09-903-456-75	Sequence 75, Appl
809	75.5	6.3	276	5	US-10-472-928-3518	Sequence 3518, Ap	882	73	6.1	272	3	US-10-156-911-75	Sequence 75, Appl
810	75.5	6.3	286	4	US-10-425-115-353980	Sequence 353980, A	883	73	6.1	272	4	US-10-812-446-75	Sequence 75, Appl
811	75.5	6.3	332	4	US-10-451-467A-5528	Sequence 528, App	884	73	6.1	272	5	US-10-333-977-5928	Sequence 5928, Ap
812	75.5	6.3	332	3	US-09-912-020-293	Sequence 293, App	885	73	6.1	322	4	US-10-177-293-160	Sequence 160, Appl
813	75.5	6.3	352	5	US-10-771-241-293	Sequence 105, App	886	73	6.1	364	4	US-10-303-204A-16	Sequence 16, Appl
814	75.5	6.3	397	5	US-10-650-467-105	Sequence 4, Appl1	887	73	6.1	377	3	US-09-939-980-53	Sequence 53, App
815	75.5	6.3	415	5	US-10-859-210-4	Sequence 107, App	888	73	6.1	450	5	US-10-626-832-59	Sequence 59, Appl
816	75.5	6.3	433	4	US-10-650-467-107	Sequence 107, App	889	73	6.1	453	4	US-10-282-122A-59343	Sequence 59343, A
817	75.5	6.3	454	4	US-10-425-115-221406	Sequence 221406, A	890	73	6.1	469	5	US-10-213-974-40	Sequence 40, Appl
818	75.5	6.3	463	4	US-10-369-493-13272	Sequence 13272, A	891	73	6.1	510	5	US-10-732-923-23538	Sequence 23538, A
819	75.5	6.3	499	5	US-10-650-467-40	Sequence 40, Appl	892	73	6.1	526	4	US-10-308-854-30	Sequence 30, Appl
820	75	6.3	349	4	US-10-437-963-169120	Sequence 169120, A	893	73	6.1	553	4	US-10-282-122A-59060	Sequence 59060, A
821	75	6.3	473	4	US-10-437-963-178A-104	Sequence 104, App	894	73	6.1	788	4	US-10-282-122A-70316	Sequence 70316, A
822	75	6.3	473	4	US-10-755-889-598	Sequence 598, App	895	73	6.1	717	6	US-09-815-242-12792	Sequence 12792, A
823	75	6.3	635	4	US-10-425-114-49467	Sequence 49467, A	896	73	6.1	748	3	US-09-746-783-86	Sequence 86, Appl
824	75	6.3	789	4	US-10-437-963-188379	Sequence 188379, A	898	73	6.1	750	3	US-10-815-242-12327	Sequence 12327, A
825	75	6.3	874	4	US-10-104-047-2866	Sequence 2866, Ap	899	73	6.1	792	3	US-09-815-242-12327	Sequence 12327, A
826	75	6.3	1131	4	US-10-104-047-2866	Sequence 86, App	900	73	6.1	792	5	US-10-470-048B-334	Sequence 334, App
827	75	6.3	2248	5	US-10-745-237-86	Sequence 20274, A	901	73	6.1	792	5	US-10-437-963-173527	Sequence 173527, A
828	75	6.3	2248	6	US-11-097-143-20274	Sequence 149181, A	902	73	6.1	806	4	US-10-450-763-54605	Sequence 54605, A
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830	74.5	6.2	355	3	US-09-789-486-4	Sequence 4, Appl1	904	73	6.1	966	5	US-10-782-695-11	Sequence 11, Appl
831	74.5	6.2	355	3	US-09-789-486-4	Sequence 3, Appl1	905	73	6.1	966	5	US-10-357-503-2	Sequence 2, Appl1
832	74.5	6.2	355	4	US-10-290-058A-3	Sequence 130, Appl	906	73	6.1	966	5	US-10-631-467-1411	Sequence 1411, Ap
833	74.5	6.2	355	4	US-10-251-385-232	Sequence 232, App	907	73	6.1	966	5	US-10-288-792-141	Sequence 141, App
834	74.5	6.2	355	4	US-10-225-567A-249	Sequence 249, App	908	73	6.1	971	5	US-10-624-727-49	Sequence 49, Appl
835	74.5	6.2	355	4	US-10-239-423-82	Sequence 82, Appl	909	73	6.1	971	5	US-10-624-727-59	Sequence 59, Appl
836	74.5	6.2	355	4	US-10-741-601-367	Sequence 367, App	910	73	6.1	971	5	US-10-756-149-5704	Sequence 5704, Ap
837	74.5	6.2	355	5	US-10-723-860-958	Sequence 958, App	911	73	6.1	971	5	US-10-450-763-36225	Sequence 36225, A
838	74.5	6.2	355	5	US-10-741-600-1084	Sequence 1084, Ap	912	73	6.1	976	5	US-10-450-763-37732	Sequence 37732, A
839	74.5	6.2	355	5	US-10-486-471-18	Sequence 18, Appl	913	73	6.1	1111	5	US-10-732-923-22531	Sequence 22531, A
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841	74.5	6.2	362	4	US-10-741-600-1085	Sequence 1085, Ap	915	73	6.1	1140	5	US-10-425-115-219168	Sequence 219168, A
842	74.5	6.2	443	4	US-10-425-115-219168	Sequence 219168, A	916	73	6.1	1140	4	US-10-425-115-232132	Sequence 232132, A

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918	72.5	6.1	209	4	US-10-080-170-107	Sequence 107, App	991	72	6.0	2307	4	US-10-191-966-2	Sequence 2, Appl
919	72.5	6.1	209	4	US-10-080-170-107	Sequence 107, App	992	72	6.0	2307	4	US-10-191-966-2	Sequence 9, Appl
920	72.5	6.1	209	4	US-10-468-356-107	Sequence 107, App	993	72	6.0	2307	4	US-10-191-966-16	Sequence 16, Appl
921	72.5	6.1	222	4	US-10-282-122A-43226	Sequence 43226, A	994	71.5	6.0	231	4	US-10-425-115-33411	Sequence 33411, Ap
922	72.5	6.1	273	4	US-10-424-599-205057	Sequence 205057, A	995	71.5	6.0	314	5	US-10-774-355A-2396	Sequence 2396, Ap
923	72.5	6.1	274	4	US-10-425-114-58050	Sequence 58050, A	996	71.5	6.0	348	4	US-10-291-253A-16	Sequence 16, Appl
924	72.5	6.1	274	4	US-10-425-114-72379	Sequence 72379, A	997	71.5	6.0	363	4	US-10-262-313-8	Sequence 8, Appl
925	72.5	6.1	274	4	US-10-424-599-187241	Sequence 187241, A	998	71.5	6.0	363	4	US-10-768-878-8	Sequence 8, Appl
926	72.5	6.1	293	4	US-10-424-599-163110	Sequence 163110, A	999	71.5	6.0	366	3	US-09-992-331-8	Sequence 8, Appl
927	72.5	6.1	307	4	US-10-425-114-66483	Sequence 66483, A	1000	71.5	6.0	382	3	US-09-971-228-5	Sequence 5, Appl
928	72.5	6.1	307	4	US-10-425-114-66808	Sequence 66808, A	1001	71.5	6.0	382	3	US-09-863-455-2	Sequence 2, Appl
929	72.5	6.1	307	4	US-10-425-114-67080	Sequence 67080, A	1002	71.5	6.0	382	3	US-09-759-514-2	Sequence 2, Appl
930	72.5	6.1	308	4	US-10-425-114-66829	Sequence 66829, A	1003	71.5	6.0	382	3	US-09-904-099-1	Sequence 1, Appl
931	72.5	6.1	310	4	US-10-425-114-66745	Sequence 66745, A	1004	71.5	6.0	382	4	US-10-425-115-238870	Sequence 238870, A
932	72.5	6.1	310	4	US-10-425-114-67361	Sequence 67361, A	1005	71.5	6.0	382	4	US-10-425-114-63895	Sequence 63895, A
933	72.5	6.1	311	4	US-10-425-114-65277	Sequence 65277, A	1006	71.5	6.0	382	4	US-10-732-923-976	Sequence 976, App
934	72.5	6.1	312	4	US-10-425-114-66761	Sequence 66761, A	1007	71.5	6.0	382	4	US-10-732-923-981	Sequence 981, App
935	72.5	6.1	312	4	US-10-425-114-66930	Sequence 66930, A	1008	71.5	6.0	382	4	US-10-437-963-181098	Sequence 181098, A
936	72.5	6.1	389	4	US-10-225-567A-215	Sequence 215, App	1009	71.5	6.0	382	5	US-10-491-545A-30	Sequence 30, Appl
937	72.5	6.1	389	4	US-10-350-924-1	Sequence 1, Appl	1010	71.5	6.0	382	5	US-10-498-848-38	Sequence 38, Appl
938	72.5	6.1	389	4	US-10-756-149-5484	Sequence 5484, Ap	1011	71.5	6.0	383	4	US-10-369-493-2267	Sequence 2267, Ap
939	72.5	6.1	448	3	US-09-935-371-16	Sequence 14, Appl	1012	71.5	6.0	390	4	US-10-775-984-3	Sequence 3, Appl
940	72.5	6.1	475	3	US-09-935-371-14	Sequence 14, Appl	1013	71.5	6.0	394	4	US-10-394-136-51	Sequence 51, Appl
941	72.5	6.1	485	3	US-09-935-371-17	Sequence 17, Appl	1014	71.5	6.0	405	4	US-10-424-599-149141	Sequence 149141, A
942	72.5	6.1	513	3	US-10-369-493-2418	Sequence 2418, Ap	1015	71.5	6.0	433	4	US-10-437-963-156065	Sequence 156065, A
943	72.5	6.1	522	4	US-10-424-599-229567	Sequence 229567, A	1016	71.5	6.0	448	4	US-10-425-114-55760	Sequence 55760, A
944	72.5	6.1	691	4	US-10-342-844-90	Sequence 90, Appl	1017	71.5	6.0	510	5	US-10-282-122A-23578	Sequence 23578, A
945	72.5	6.1	769	4	US-09-882-986-2	Sequence 2, Appl	1018	71.5	6.0	524	4	US-10-282-122A-53957	Sequence 53957, A
946	72.5	6.1	848	3	US-10-469-013-18	Sequence 18, Appl	1019	71.5	6.0	538	4	US-10-424-599-248196	Sequence 248196, A
947	72.5	6.1	848	4	US-10-740-084-2	Sequence 2, Appl	1020	71.5	6.0	555	4	US-10-176-847-100	Sequence 100, App
948	72.5	6.1	851	4	US-10-282-122A-53083	Sequence 2, Appl	1021	71.5	6.0	558	3	US-09-843-856-2	Sequence 2, Appl
949	72.5	6.1	899	4	US-10-425-115-200708	Sequence 53083, A	1022	71.5	6.0	568	3	US-10-282-122A-44316	Sequence 44316, A
950	72.5	6.1	903	4	US-10-425-114-65959	Sequence 65959, A	1023	71.5	6.0	603	4	US-09-371-347-48	Sequence 48, Appl
951	72.5	6.1	1051	5	US-10-886-773-4	Sequence 4, Appl	1024	71.5	6.0	669	3	US-11-119-096-46	Sequence 46, Appl
952	72.5	6.1	1707	4	US-10-437-963-167354	Sequence 167354, A	1025	71.5	6.0	697	6	US-09-371-347-46	Sequence 46, Appl
953	72.5	6.1	223	4	US-10-437-963-154005	Sequence 154005, A	1026	71.5	6.0	697	6	US-11-119-096-46	Sequence 46, Appl
954	72.5	6.0	254	4	US-10-017-161-570	Sequence 570, App	1027	71.5	6.0	698	3	US-09-371-347-21	Sequence 21, Appl
955	72.5	6.0	311	5	US-10-774-355A-2017	Sequence 2017, Ap	1028	71.5	6.0	698	3	US-09-371-347-42	Sequence 42, Appl
956	72.5	6.0	334	3	US-09-925-289-932	Sequence 932, App	1029	71.5	6.0	698	3	US-09-371-347-44	Sequence 44, Appl
957	72.5	6.0	334	3	US-10-282-122A-67356	Sequence 67356, A	1030	71.5	6.0	698	5	US-10-741-600-1520	Sequence 1520, Ap
958	72.5	6.0	334	3	US-09-925-289-932	Sequence 932, App	1031	71.5	6.0	698	5	US-10-450-763-31242	Sequence 31242, A
959	72.5	6.0	334	3	US-10-424-599-184842	Sequence 184842, A	1032	71.5	6.0	698	5	US-11-119-096-2	Sequence 2, Appl
960	72.5	6.0	338	4	US-10-335-977-5639	Sequence 5639, Ap	1033	71.5	6.0	698	6	US-11-119-096-21	Sequence 21, Appl
961	72.5	6.0	375	4	US-10-282-122A-47856	Sequence 47856, A	1034	71.5	6.0	698	6	US-11-119-096-42	Sequence 42, Appl
962	72.5	6.0	414	5	US-10-450-763-55410	Sequence 55410, A	1035	71.5	6.0	698	6	US-11-119-096-44	Sequence 44, Appl
963	72.5	6.0	448	6	US-11-097-143-15498	Sequence 15498, A	1036	71.5	6.0	698	6	US-10-741-600-1521	Sequence 1521, Ap
964	72.5	6.0	453	5	US-10-282-122A-44365	Sequence 44365, A	1037	71.5	6.0	725	5	US-10-732-923-23563	Sequence 23563, A
965	72.5	6.0	453	5	US-10-470-048B-59	Sequence 59, Appl	1038	71.5	6.0	743	5	US-10-060-425-2	Sequence 2, Appl
966	72.5	6.0	453	5	US-10-732-923-9790	Sequence 9790, Ap	1039	71.5	6.0	890	4	US-10-276-774-1774	Sequence 1774, Ap
967	72.5	6.0	543	5	US-10-369-493-12601	Sequence 12601, A	1040	71.5	6.0	2923	3	US-09-788-711A-3	Sequence 4, Appl
968	72.5	6.0	552	4	US-10-287-122A-53662	Sequence 53662, A	1041	71.5	6.0	2923	3	US-09-916-849A-3	Sequence 3, Appl
969	72.5	6.0	594	4	US-10-408-765A-1189	Sequence 1189, Ap	1042	71.5	6.0	2923	4	US-10-225-567A-524	Sequence 524, App
970	72.5	6.0	696	4	US-10-225-567A-424	Sequence 424, App	1043	71.5	6.0	2923	4	US-10-174-677-29	Sequence 29, Appl
971	72.5	6.0	696	4	US-10-241-220-83	Sequence 83, Appl	1044	71.5	6.0	2923	4	US-10-120-801-53	Sequence 53, Appl
972	72.5	6.0	696	4	US-10-241-220-83	Sequence 83, Appl	1045	71.5	6.0	2923	4	US-10-292-798-932	Sequence 92, App
973	72.5	6.0	696	5	US-10-872-972-83	Sequence 83, Appl	1046	71.5	6.0	2923	4	US-10-038-954-70	Sequence 9, Appl
974	72.5	6.0	696	5	US-10-872-972-84	Sequence 83, Appl	1047	71.5	6.0	2923	4	US-10-311-623-9	Sequence 9, Appl
975	72.5	6.0	696	5	US-10-872-991-83	Sequence 83, Appl	1048	71.5	6.0	2923	4	US-10-097-143-30330	Sequence 30330, A
976	72.5	6.0	696	5	US-10-872-991-84	Sequence 84, Appl	1049	71.5	6.0	2923	4	US-10-474-792-346	Sequence 346, App
977	72.5	6.0	696	5	US-10-756-149-5432	Sequence 5432, Ap	1050	71.5	6.0	2923	5	US-10-425-114-36801	Sequence 36801, A
978	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1051	71.5	6.0	2923	5	US-10-425-115-238819	Sequence 238819, A
979	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1052	71.5	6.0	2923	5	US-10-425-115-238870	Sequence 238870, A
980	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1053	71.5	6.0	2923	5	US-10-425-115-238870	Sequence 238870, A
981	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1054	71.5	6.0	2923	5	US-10-425-115-238870	Sequence 238870, A
982	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1055	71.5	6.0	2923	5	US-10-425-115-238870	Sequence 238870, A
983	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1056	71.5	6.0	2923	5	US-10-425-115-238870	Sequence 238870, A
984	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1057	71.5	6.0	2923	5	US-10-425-115-238870	Sequence 238870, A
985	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1058	71.5	6.0	2923	5	US-10-425-115-238870	Sequence 238870, A
986	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1059	71.5	6.0	2923	5	US-10-425-115-238870	Sequence 238870, A
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988	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1061	71.5	6.0	2923	5	US-10-425-115-238870	Sequence 238870, A
989	72.5	6.0	741	4	US-10-270-875-11	Sequence 11, Appl	1062	71.5	6.0	2923	5	US-10-425-115-238870	Sequence 238870, A

1063	71	5.9	444	US-10-287-226-372	Sequence 372, App	1136	70.5	5.9	433	US-10-354-247-20	Sequence 20, Appl
1064	71	5.9	451	US-10-733-923-4838	Sequence 4838, Ap	1137	70.5	5.9	480	US-09-895-912A-9-32	Sequence 92, Appl
1065	71	5.9	457	US-10-282-132A-47836	Sequence 47836, A	1138	70.5	5.9	494	US-10-425-111-65620	Sequence 65620, A
1066	71	5.9	470	US-10-166-101-8	Sequence 8, Appl1	1139	70.5	5.9	499	US-10-724-972A-5387	Sequence 5387, Ap
1067	71	5.9	470	US-10-176-255-25	Sequence 25, Appl	1140	70.5	5.9	521	US-10-282-122A-58397	Sequence 58397, A
1068	71	5.9	470	US-10-055-555-25	Sequence 25, Appl	1141	70.5	5.9	539	US-10-051-902-26	Sequence 26, Appl
1069	71	5.9	470	US-10-980-560-25	Sequence 25, Appl	1142	70.5	5.9	539	US-10-051-909-26	Sequence 26, Appl
1070	71	5.9	471	US-08-681-219-30	Sequence 21, Appl	1143	70.5	5.9	548	US-10-282-122A-55342	Sequence 55342, A
1071	71	5.9	471	US-09-929-313-2	Sequence 2, Appl1	1144	70.5	5.9	556	US-10-369-499-5442	Sequence 5442, Ap
1072	71	5.9	471	US-09-230-111C-28	Sequence 28, Appl	1145	70.5	5.9	559	US-10-845-900-11	Sequence 11, Appl
1073	71	5.9	471	US-10-251-385-122	Sequence 122, App	1146	70.5	5.9	717	US-09-925-300-1199	Sequence 1299, Ap
1074	71	5.9	471	US-10-251-385-228	Sequence 228, App	1147	70.5	5.9	740	US-10-051-903-37	Sequence 37, Appl
1075	71	5.9	471	US-10-225-567A-12	Sequence 12, App	1148	70.5	5.9	740	US-10-437-963-15955	Sequence 15955, Sequence 135677,
1076	71	5.9	471	US-10-318-661-22	Sequence 22, Appl	1149	70.5	5.9	796	US-10-437-963-155677	Sequence 7591, Ap
1077	71	5.9	471	US-10-092-138-28	Sequence 28, Appl	1150	70.5	5.9	1026	US-10-032-588-7591	Sequence 22552, A
1078	71	5.9	471	US-10-820-403-28	Sequence 28, Appl	1151	70.5	5.9	1158	US-10-732-922-22552	Sequence 44, Appl
1079	71	5.9	471	US-10-741-600-1461	Sequence 1461, Ap	1152	70.5	5.9	1163	US-10-336-472-4	Sequence 4, Appl1
1080	71	5.9	471	US-10-741-600-1462	Sequence 1462, Ap	1153	70.5	5.9	1781	US-09-738-877-3	Sequence 3, Appl1
1081	71	5.9	471	US-10-741-600-1463	Sequence 1463, Ap	1154	70.5	5.9	1781	US-09-961-403-13	Sequence 13, Appl
1082	71	5.9	471	US-10-895-789-22	Sequence 22, Appl	1155	70.5	5.9	1781	US-10-428-487-16	Sequence 16, Appl
1083	71	5.9	473	US-10-335-977-5539	Sequence 5539, Ap	1156	70.5	5.9	1781	US-10-211-462-44	Sequence 44, Appl
1084	71	5.9	495	US-10-437-963-20163	Sequence 20163, Sequence 22014, A	1157	70.5	5.9	1787	US-10-732-922-8682	Sequence 8682, Ap
1085	71	5.9	546	US-10-369-493-22014	Sequence 22014, A	1158	70.5	5.9	1795	US-10-450-763-51377	Sequence 51377, A
1086	71	5.9	559	US-10-128-714-8457	Sequence 8457, Ap	1159	70.5	5.9	226	US-10-501-282-3730	Sequence 3730, Ap
1087	71	5.9	563	US-10-149-310-236	Sequence 236, App	1160	70	5.9	256	US-10-795-159-739	Sequence 739, App
1088	71	5.9	564	US-10-968-848-83	Sequence 83, Appl	1161	70	5.9	256	US-11-097-143-36162	Sequence 36162, A
1089	71	5.9	629	US-10-437-963-119462	Sequence 119462, Sequence 119462, Appl1	1162	70	5.9	292	US-10-282-122A-63601	Sequence 63601, A
1090	71	5.9	727	US-10-319-315-1	Sequence 1, Appl1	1163	70	5.9	309	US-09-864-022-34	Sequence 34, Appl
1091	71	5.9	727	US-10-114-270-190	Sequence 1270, App	1164	70	5.9	311	US-09-908-006A-41	Sequence 41, Appl
1092	71	5.9	788	US-10-335-977-5540	Sequence 1590, App	1165	70	5.9	311	US-09-908-006A-44	Sequence 44, Appl
1093	71	5.9	792	US-11-097-143-6948	Sequence 6948, Ap	1166	70	5.9	333	US-10-251-385-116	Sequence 16, Appl
1094	71	5.9	862	US-10-437-963-141086	Sequence 141086, Sequence 131174, A	1167	70	5.9	333	US-10-251-385-1172	Sequence 172, Appl
1095	71	5.9	932	US-10-437-963-131174	Sequence 131174, Sequence 186252, A	1168	70	5.9	333	US-10-425-567A-279	Sequence 279, App
1096	71	5.9	1738	US-10-437-963-186252	Sequence 186252, Sequence 27, Appl	1169	70	5.9	333	US-10-433-561-32	Sequence 32, Appl
1097	71	5.9	2296	US-10-952-915-27	Sequence 27, Appl	1170	70	5.9	333	US-10-477-728-4	Sequence 4, Appl1
1098	70.5	5.9	147	US-10-767-701-60641	Sequence 60641, A	1171	70	5.9	333	US-10-480-733A-84	Sequence 84, Appl
1099	70.5	5.9	202	US-10-501-071-40	Sequence 40, Appl	1172	70	5.9	333	US-10-723-860-27338	Sequence 2738, Ap
1100	70.5	5.9	218	US-10-115-571A-64	Sequence 64, Appl	1173	70	5.9	333	US-10-788-197-75	Sequence 75, Appl
1101	70.5	5.9	228	US-10-051-902-16	Sequence 16, Appl	1174	70	5.9	333	US-10-788-197-75	Sequence 75, Appl
1102	70.5	5.9	228	US-10-051-909-16	Sequence 16, Appl	1175	70	5.9	333	US-10-311-028B-4	Sequence 4, Appl1
1103	70.5	5.9	235	US-10-425-115-225051	Sequence 235051, Sequence 45354, A	1176	70	5.9	339	US-10-767-701-42928	Sequence 42928, A
1104	70.5	5.9	275	US-10-282-122A-45354	Sequence 45354, A	1177	70	5.9	347	US-10-788-197-77	Sequence 77, Appl
1105	70.5	5.9	279	US-10-767-701-45405	Sequence 45405, A	1178	70	5.9	364	US-10-633-438-56	Sequence 56, Appl
1106	70.5	5.9	283	US-10-425-114-62068	Sequence 62068, A	1179	70	5.9	364	US-10-788-197-79	Sequence 79, Appl
1107	70.5	5.9	314	US-10-437-963-191259	Sequence 191259, Sequence 158, App	1180	70	5.9	364	US-10-901-772-56	Sequence 56, Appl
1108	70.5	5.9	343	US-10-403-142-158	Sequence 158, App	1181	70	5.9	378	US-10-788-197-81	Sequence 81, Appl
1109	70.5	5.9	363	US-10-262-313-9	Sequence 9, Appl1	1182	70	5.9	388	US-10-334-360-13	Sequence 13, Appl
1110	70.5	5.9	363	US-10-768-878-9	Sequence 9, Appl1	1183	70	5.9	399	US-10-094-749-1578	Sequence 178, Ap
1111	70.5	5.9	365	US-10-060-902-32	Sequence 32, Appl	1184	70	5.9	471	US-09-989-861-17	Sequence 17, Appl
1112	70.5	5.9	365	US-10-354-247-32	Sequence 32, Appl	1185	70	5.9	475	US-10-297-022-24	Sequence 24, Appl
1113	70.5	5.9	366	US-09-992-331-9	Sequence 9, Appl1	1186	70	5.9	513	US-10-424-589-195511	Sequence 195511, Sequence 20, Appl
1114	70.5	5.9	366	US-10-369-493-10462	Sequence 10462, A	1187	70	5.9	540	US-10-343-902-20	Sequence 20, Appl
1115	70.5	5.9	374	US-10-060-902-30	Sequence 30, Appl	1188	70	5.9	602	US-10-282-122A-6186	Sequence 6186, A
1116	70.5	5.9	374	US-10-354-247-30	Sequence 30, Appl	1189	70	5.9	637	US-10-282-122A-61377	Sequence 61377, A
1117	70.5	5.9	388	US-10-060-902-16	Sequence 16, Appl	1190	70	5.9	640	US-09-769-736-123	Sequence 123, App
1118	70.5	5.9	388	US-10-354-247-16	Sequence 16, Appl	1191	70	5.9	758	US-10-425-113-337864	Sequence 327864, A
1119	70.5	5.9	390	US-10-060-902-22	Sequence 22, Appl	1192	70	5.9	1003	US-10-732-922-22128	Sequence 22128, A
1120	70.5	5.9	390	US-10-060-902-22	Sequence 22, Appl	1193	70	5.9	1041	US-10-369-493-11095	Sequence 11095, A
1121	70.5	5.9	390	US-10-354-247-22	Sequence 22, Appl	1194	70	5.9	1053	US-10-732-922-1134	Sequence 1734, Ap
1122	70.5	5.9	393	US-10-354-247-24	Sequence 24, Appl	1195	70	5.9	1236	US-10-425-115-213298	Sequence 213298, Sequence 118551,
1123	70.5	5.9	393	US-10-060-902-28	Sequence 28, Appl	1196	70	5.9	2738	US-10-437-963-118551	Sequence 41, Appl
1124	70.5	5.9	393	US-10-060-902-36	Sequence 36, Appl	1197	70	5.8	141	US-10-115-571A-41	Sequence 41, Appl
1125	70.5	5.9	393	US-10-354-247-28	Sequence 28, Appl	1198	70	5.8	141	US-10-732-922-4771	Sequence 4771, Ap
1126	70.5	5.9	393	US-10-354-247-36	Sequence 36, Appl	1199	70	5.8	201	US-10-501-282-3216	Sequence 3216, Ap
1127	70.5	5.9	402	US-10-225-567A-294	Sequence 294, App	1200	70	5.8	210	US-09-811-284-158	Sequence 198, App
1128	70.5	5.9	402	US-10-060-902-34	Sequence 34, Appl	1201	70	5.8	247	US-10-501-282-3218	Sequence 3218, Ap
1129	70.5	5.9	407	US-10-354-247-34	Sequence 34, Appl	1202	70	5.8	253	US-09-981-566A-51	Sequence 51, Appl
1130	70.5	5.9	407	US-10-060-902-18	Sequence 18, Appl	1203	69.5	5.8	257	US-10-767-701-45706	Sequence 45706, A
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1132	70.5	5.9	421	US-10-425-115-257457	Sequence 257457, Sequence 26, Appl	1205	69.5	5.8	293	US-10-156-761-12630	Sequence 12630, A
1133	70.5	5.9	425	US-10-060-902-26	Sequence 26, Appl	1206	69.5	5.8	296	US-10-402-84-24	Sequence 24, Appl
1134	70.5	5.9	425	US-10-354-247-26	Sequence 26, Appl	1207	69.5	5.8	296	US-10-746-795-24	Sequence 24, Appl
1135	70.5	5.9	433	US-10-060-902-20	Sequence 20, Appl	1208	69.5	5.8	306	US-10-425-115-152496	Sequence 152496, Sequence 192496,

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1210	69.5	5.8	308	3	US-09-804-291-453	Sequence 453, App	1283	69	5.8	388	4	US-10-282-122A-42742	Sequence 42742, A
1211	69.5	5.8	308	4	US-10-017-161-912	Sequence 912, App	1284	69	5.8	388	5	US-10-771-241-378	Sequence 378, App
1212	69.5	5.8	308	4	US-10-044-643-9	Sequence 9, App1	1285	69	5.8	434	4	US-10-424-599-283401	Sequence 283401, A
1213	69.5	5.8	308	4	US-10-292-798-786	Sequence 786, App	1286	69	5.8	437	4	US-10-369-493-23659	Sequence 23659, A
1214	69.5	5.8	308	4	US-10-343-650A-216	Sequence 216, App	1287	69	5.8	451	4	US-10-424-599-184025	Sequence 184025, A
1215	69.5	5.8	308	5	US-10-819-316-453	Sequence 453, App	1288	69	5.8	467	4	US-10-425-115-368834	Sequence 368834, A
1216	69.5	5.8	321	4	US-10-289-762-778	Sequence 778, App	1289	69	5.8	488	4	US-10-425-115-195408	Sequence 195408, A
1217	69.5	5.8	321	4	US-10-425-115-257455	Sequence 257455, A	1290	69	5.8	515	4	US-10-424-599-229564	Sequence 229564, A
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1220	69.5	5.8	400	4	US-10-282-122A-60622	Sequence 60622, App	1293	69	5.8	591	4	US-10-437-963-163509	Sequence 163509, A
1221	69.5	5.8	415	6	US-11-097-143-9636	Sequence 9636, App	1294	69	5.8	593	6	US-11-097-143-6072	Sequence 6072, App
1222	69.5	5.8	421	4	US-10-156-761-14096	Sequence 14096, A	1295	69	5.8	642	4	US-10-437-963-150528	Sequence 150528, A
1223	69.5	5.8	428	6	US-11-097-143-27768	Sequence 27768, A	1296	69	5.8	666	4	US-10-276-77A-2139	Sequence 2139, App
1224	69.5	5.8	461	5	US-10-617-320-3722	Sequence 3722, App	1297	69	5.8	742	4	US-10-424-599-251277	Sequence 251277, A
1225	69.5	5.8	477	4	US-10-369-493-5002	Sequence 5002, App	1298	69	5.8	756	4	US-10-425-115-54335	Sequence 54335, A
1226	69.5	5.8	477	5	US-10-732-923-4293	Sequence 4293, App	1299	69	5.8	875	4	US-10-363-616-397	Sequence 397, App
1227	69.5	5.8	490	4	US-10-369-493-17545	Sequence 17545, A	1300	69	5.8	1058	5	US-10-732-923-22426	Sequence 22426, A
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1229	69.5	5.8	531	4	US-10-425-115-293577	Sequence 293577, A	1302	69	5.8	2310	3	US-09-995-542-10	Sequence 10, App1
1230	69.5	5.8	540	4	US-10-354-437-54	Sequence 54, App1	1303	69	5.8	5127	4	US-10-668-767-8	Sequence 8, App1
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1234	69.5	5.8	557	4	US-10-762-154-3	Sequence 3, App1	1307	68.5	5.7	174	4	US-10-767-701-32984	Sequence 32984, A
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1236	69.5	5.8	557	5	US-10-940-500-1	Sequence 1, App1	1309	68.5	5.7	200	4	US-10-428-826-36	Sequence 36, App1
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1238	69.5	5.8	568	4	US-10-264-237-2041	Sequence 2041, App	1311	68.5	5.7	209	4	US-10-958-863-86	Sequence 86, App1
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1247	69.5	5.8	801	4	US-10-282-122A-71745	Sequence 71745, A	1320	68.5	5.7	327	5	US-10-478-677-13	Sequence 13, App1
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1253	69.5	5.8	1704	4	US-10-336-215-120	Sequence 120, App	1326	68.5	5.7	377	5	US-10-732-923-4899	Sequence 2, App1
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1256	69.5	5.8	1704	4	US-10-648-593-713	Sequence 276554, A	1329	68.5	5.7	383	6	US-11-100-593-8	Sequence 8, App1
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1260	69.5	5.8	213	5	US-10-732-923-5075	Sequence 5075, App	1333	68.5	5.7	444	3	US-09-853-386-136	Sequence 136, App
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1265	69.5	5.8	283	4	US-10-425-115-333413	Sequence 333413, A	1338	68.5	5.7	448	3	US-09-935-371-22	Sequence 22, App1
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1268	69.5	5.8	306	4	US-10-787-098-9	Sequence 9, App1	1341	68.5	5.7	468	5	US-10-925-095-553	Sequence 553, App
1269	69.5	5.8	321	5	US-10-774-355A-2034	Sequence 2034, App	1342	68.5	5.7	475	3	US-09-935-371-24	Sequence 24, App1
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1279	69.5	5.8	380	4	US-11-116-727-46	Sequence 46, App	1352	68.5	5.7	502	4	US-10-225-567A-231	Sequence 231, App
1280	69.5	5.8	380	4	US-10-611-210-11	Sequence 11, App1	1353	68.5	5.7	502	4	US-10-225-567A-231	Sequence 231, App
1281	69.5	5.8	388	3	US-09-741-669-370	Sequence 370, App	1354	68.5	5.7	502	4	US-10-225-567A-231	Sequence 231, App



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1357	68.5	5.7	548	3	US-09-882-171-469	Sequence 469, App	1430	68	5.7	355	3	US-09-960-547-1	Sequence 1, Appli
1358	68.5	5.7	548	4	US-10-164-861-469	Sequence 469, App	1431	68	5.7	355	3	US-09-886-1192A-14	Sequence 14, Appl
1359	68.5	5.7	548	4	US-10-440-464-88	Sequence 88, Appl	1432	68	5.7	355	3	US-09-893-512-11	Sequence 11, Appl
1360	68.5	5.7	552	3	US-09-935-371-27	Sequence 27, Appl	1433	68	5.7	355	3	US-10-039-659-13	Sequence 13, Appl
1361	68.5	5.7	553	3	US-09-935-371-25	Sequence 25, Appl	1434	68	5.7	355	4	US-10-225-674-62	Sequence 62, Appl
1362	68.5	5.7	553	3	US-09-935-371-29	Sequence 29, Appl	1435	68	5.7	355	4	US-10-245-850-2	Sequence 2, Appli
1363	68.5	5.7	553	3	US-10-424-599-253232	Sequence 253232, A	1436	68	5.7	355	4	US-10-376-564-14	Sequence 14, Appl
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1367	68.5	5.7	670	5	US-10-739-930-10578	Sequence 10578, A	1440	68	5.7	355	4	US-10-754-071-13	Sequence 13, Appl
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1375	68.5	5.7	1178	4	US-10-320-797-3347	Sequence 3347, Ap	1448	68	5.7	355	5	US-10-759-860-13	Sequence 13, Appl
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1377	68.5	5.7	1236	4	US-10-208-731-9	Sequence 9, Appli	1450	68	5.7	355	5	US-10-799-736-11	Sequence 11, Appl
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1379	68	5.7	143	4	US-10-767-701-36814	Sequence 36814, A	1452	68	5.7	355	5	US-10-734-692-6	Sequence 6, Appli
1380	68	5.7	247	3	US-09-738-626-5109	Sequence 5109, Ap	1453	68	5.7	355	5	US-10-734-692-6	Sequence 6, Appli
1381	68	5.7	258	4	US-10-023-171-7	Sequence 7, Appli	1454	68	5.7	355	6	US-11-021-691-160	Sequence 160, App
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1384	68	5.7	273	6	US-11-083-611-85	Sequence 85, Appl	1457	68	5.7	375	4	US-10-219-834-78	Sequence 78, Appl
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1393	68	5.7	330	3	US-09-991-225-2	Sequence 2, Appli	1466	68	5.7	471	3	US-09-951-217-8	Sequence 8, Appli
1394	68	5.7	330	4	US-10-369-405-2	Sequence 2, Appli	1467	68	5.7	471	5	US-10-032-585-7028	Sequence 7028, Ap
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1396	68	5.7	341	3	US-09-991-225-55	Sequence 55, Appl	1469	68	5.7	471	5	US-10-777-195-8	Sequence 8, Appli
1397	68	5.7	341	3	US-10-369-405-55	Sequence 55, Appl	1470	68	5.7	471	5	US-10-882-104-88	Sequence 88, Appl
1398	68	5.7	346	3	US-09-826-791-6	Sequence 6, Appli	1471	68	5.7	472	3	US-09-951-217-8	Sequence 36, Appl
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1405	68	5.7	346	3	US-09-980-049-1	Sequence 1, Appli	1478	68	5.7	488	4	US-10-295-027-1326	Sequence 1326, App
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1410	68	5.7	346	4	US-10-131-332A-2	Sequence 2, Appli	1483	68	5.7	490	4	US-10-450-763-56651	Sequence 56651, A
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1415	68	5.7	346	4	US-10-343-650A-58	Sequence 58, Appl	1488	68	5.7	562	4	US-10-275-026A-92	Sequence 92, Appl
1416	68	5.7	346	4	US-10-297-247-2	Sequence 2, Appli	1489	68	5.7	562	4	US-10-369-493-4101	Sequence 4101, Ap
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1425	68	5.7	346	5	US-10-435-828-2	Sequence 18, Appl	1498	68	5.7	799	4	US-10-788-266-2	Sequence 18, Appl
1426	68	5.7	346	5	US-10-930-662-14	Sequence 14, Appl	1499	68	5.7	804	5	US-10-732-923-17416	Sequence 17416, A
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#### SUMMARIES

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107	70	5.9	383	11	US-11-096-5684-22839	Sequence 22839, A	180	67.5	5.6	2804	11	US-11-120-923-3	Sequence 3, Appl1
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154	68.5	5.7	599	11	US-11-124-367A-392	Sequence 392, App	227	65.5	5.5	617	11	US-11-045-004-200	Sequence 200, App
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168	67.5	5.6	226	11	US-11-188-298-1316	Sequence 1316, Ap	241	65	5.4	461	9	US-10-784-004-685	Sequence 685, App
169	67.5	5.6	286	11	US-11-096-5684-8161	Sequence 8161, Ap	242	65	5.4	461	9	US-10-784-004-1071	Sequence 1071, App
170	67.5	5.6	292	11	US-11-096-5684-15102	Sequence 15102, A	243	65	5.4	480	9	US-10-467-657-3124	Sequence 3124, Ap
171	67.5	5.6	321	11	US-11-096-5684-15101	Sequence 15101, A	244	65	5.4	600	9	US-10-467-657-4866	Sequence 4866, Ap
172	67.5	5.6	339	11	US-11-188-298-2603	Sequence 2603, A	245	65	5.4	718	11	US-11-096-5684-26497	Sequence 26497, A
173	67.5	5.6	350	9	US-10-515-604-2	Sequence 2, Appl1	246	65	5.4	1220	11	US-11-079-463-7103	Sequence 7103, Ap
174	67.5	5.6	354	11	US-11-096-5684-15100	Sequence 15100, A	247	64.5	5.4	213	11	US-11-096-5684-29542	Sequence 29542, A

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250	64.5	5.4	311	11	US-11-188-298-10501	Sequence 10501, A	328	63	5.3	172	11	US-11-079-463-6028	Sequence 6028, Ap
251	64.5	5.4	314	11	US-11-055-822-284	Sequence 284, App	329	63	5.3	178	9	US-10-507-355-5	Sequence 5, App1
252	64.5	5.4	324	11	US-11-079-463-6638	Sequence 6638, Ap	330	63	5.3	178	11	US-11-087-099-11791	Sequence 1791, Ap
253	64.5	5.4	400	9	US-10-499-210-2	Sequence 2, App1	331	63	5.3	178	11	US-11-087-099-11170	Sequence 11170, A
254	64.5	5.4	416	11	US-11-045-004-473	Sequence 473, App	332	63	5.3	259	9	US-10-055-877-225	Sequence 225, App
255	64.5	5.4	450	9	US-10-507-720-18	Sequence 18, App1	333	63	5.3	229	9	US-10-055-877-2237	Sequence 237, App
256	64.5	5.4	486	11	US-11-210-316-10	Sequence 10, App1	334	63	5.3	229	11	US-11-206-587-27	Sequence 27, App1
257	64.5	5.4	495	9	US-10-508-263-20	Sequence 20, App1	335	63	5.3	229	11	US-11-206-587-29	Sequence 29, App1
258	64.5	5.4	567	11	US-11-120-422-7	Sequence 7, App1	336	63	5.3	273	11	US-11-206-587-34	Sequence 34, App1
259	64.5	5.4	622	11	US-11-045-004-780	Sequence 780, App	337	63	5.3	220	11	US-11-188-298-348	Sequence 348, App
260	64.5	5.4	629	11	US-11-232-006A-24	Sequence 24, App1	338	63	5.3	332	11	US-11-096-568A-28678	Sequence 28678, A
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262	64.5	5.4	747	11	US-11-210-316-2	Sequence 2, App1	340	63	5.3	332	11	US-11-172-740-976	Sequence 976, App
263	64.5	5.4	847	11	US-11-087-099-1706	Sequence 1706, Ap	341	63	5.3	339	11	US-11-172-740-976	Sequence 28677, A
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266	64	5.4	235	11	US-11-087-099-3045	Sequence 3045, Ap	344	63	5.3	339	9	US-10-793-626-2426	Sequence 2426, Ap
267	64	5.4	239	9	US-10-895-064-1311	Sequence 1311, Ap	345	63	5.3	388	11	US-11-046-668-7	Sequence 7, App1
268	64	5.4	239	9	US-11-129-741-1311	Sequence 1311, Ap	346	63	5.3	381	11	US-11-188-298-14752	Sequence 14752, A
269	64	5.4	244	11	US-11-087-099-1135	Sequence 1135, App	347	63	5.3	391	11	US-11-096-568A-15310	Sequence 15310, A
270	64	5.4	331	11	US-11-172-740-979	Sequence 979, App	348	63	5.3	410	11	US-11-096-568A-15309	Sequence 7, App1
271	64	5.4	402	11	US-11-045-004-1429	Sequence 1429, App	349	63	5.3	415	11	US-11-199-821-7	Sequence 31010, A
272	64	5.4	422	11	US-11-087-099-9711	Sequence 9711, Ap	350	63	5.3	422	11	US-11-096-568A-31010	Sequence 13929, A
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278	64	5.4	479	11	US-11-098-686-10838	Sequence 10838, A	356	63	5.3	450	11	US-11-232-805-27	Sequence 28676, A
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282	64	5.4	512	11	US-11-188-298-7971	Sequence 7971, Ap	360	63	5.3	508	9	US-10-980-388-112	Sequence 12, App1
283	64	5.4	534	9	US-10-793-626-920	Sequence 920, App	361	63	5.3	509	11	US-11-055-309A-12	Sequence 219, App
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297	64	5.4	1462	9	US-10-501-035-277	Sequence 277, App	380	62.5	5.2	371	11	US-11-188-298-13966	Sequence 9945, App
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299	63.5	5.3	334	11	US-11-096-568A-6294	Sequence 6294, Ap	382	62.5	5.2	376	11	US-11-188-298-9945	Sequence 6199, Ap
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301	63.5	5.3	380	9	US-10-784-004-351	Sequence 351, App	384	62.5	5.2	439	11	US-11-096-568A-6198	Sequence 6197, Ap
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313	63.5	5.3	568	11	US-11-228-079-10	Sequence 10, App1	392	62.5	5.2	470	11	US-11-188-298-12101	Sequence 30130, A
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316	63.5	5.3	632	11	US-11-188-298-1895	Sequence 1895, Ap	395	62.5	5.2	479	11	US-11-188-298-9712	Sequence 298, App
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321	63.5	5.3	685	9	US-10-506-454-321	Sequence 321, App	400	62.5	5.2	609	9	US-10-511-538-253	
322	63.5	5.3	768	11	US-11-079-463-5510	Sequence 5510, Ap	401	62.5	5.2	668	11	US-10-511-538-253	
323	63.5	5.3	775	9	US-10-453-372-656	Sequence 656, App	402	62.5	5.2	668	11	US-11-188-298-20527	
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325	63.5	5.3	1208	9	US-10-330-773-810	Sequence 810, App							

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405	62.5	5.2	1144	9	US-10-467-657-1820	Sequence 1820, Ap	481	61.5	5.1	490	11	US-11-068-859-75	Sequence 75, Appl
406	62.5	5.2	3375	11	US-11-044-111-23	Sequence 23, Appl	482	61.5	5.1	490	11	US-11-068-859-77	Sequence 77, Appl
407	62	5.2	177	11	US-11-087-099-11875	Sequence 11875, A	483	61.5	5.1	490	11	US-11-068-859-81	Sequence 81, Appl
408	62	5.2	188	11	US-11-096-568A-18452	Sequence 18452, A	484	61.5	5.1	490	11	US-11-068-859-83	Sequence 83, Appl
409	62	5.2	158	11	US-11-096-568A-18451	Sequence 18451, A	485	61.5	5.1	490	11	US-11-068-859-87	Sequence 87, Appl
410	62	5.2	249	11	US-11-087-099-1059	Sequence 1059, Ap	486	61.5	5.1	490	11	US-11-068-859-100	Sequence 100, Appl
411	62	5.2	247	11	US-11-045-004-1955	Sequence 1955, Ap	487	61.5	5.1	490	11	US-11-068-859-180	Sequence 180, Appl
412	62	5.2	272	10	US-11-024-544A-120	Sequence 120, App	488	61.5	5.1	490	11	US-11-068-859-190	Sequence 190, Appl
413	62	5.2	272	10	US-11-024-545-48	Sequence 48, Appl	489	61.5	5.1	490	11	US-11-068-859-192	Sequence 192, Appl
414	62	5.2	272	10	US-11-185-301-36	Sequence 36, Appl	490	61.5	5.1	490	11	US-11-068-859-196	Sequence 196, Appl
415	62	5.2	272	10	US-11-190-750-103	Sequence 103, App	491	61.5	5.1	506	11	US-11-013-592-8	Sequence 8, Appl1
416	62	5.2	272	10	US-11-251-466-22	Sequence 22, Appl	492	61.5	5.1	557	11	US-11-087-099-11351	Sequence 11351, A
417	62	5.2	272	10	US-11-254-173-36	Sequence 36, Appl	493	61.5	5.1	557	11	US-11-087-099-11163	Sequence 11163, A
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419	62	5.2	272	11	US-11-146-428-58	Sequence 58, Appl	495	61.5	5.1	616	11	US-11-096-568A-13957	Sequence 33957, A
420	62	5.2	272	11	US-11-225-354-29	Sequence 29, Appl	496	61.5	5.1	634	11	US-11-188-298-21043	Sequence 21043, A
421	62	5.2	313	9	US-10-055-877-234	Sequence 234, App	497	61.5	5.1	679	11	US-11-188-298-21626	Sequence 21626, A
422	62	5.2	313	11	US-11-096-568A-18450	Sequence 18450, A	498	61.5	5.1	679	11	US-11-072-175-214	Sequence 214, App
423	62	5.2	353	11	US-11-017-058-9	Sequence 9, Appl1	499	61.5	5.1	679	11	US-11-079-463-9258	Sequence 9258, App
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433	62	5.2	447	11	US-11-096-568A-32556	Sequence 32556, A	509	61	5.1	122	9	US-11-087-099-8902	Sequence 8902, App
434	62	5.2	456	9	US-10-467-657-4150	Sequence 4150, Ap	510	61	5.1	122	9	US-11-087-099-11390	Sequence 11390, A
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436	62	5.2	514	9	US-10-511-538-48	Sequence 48, Appl	512	61	5.1	200	9	US-10-793-626-1242	Sequence 1242, Ap
437	62	5.2	514	11	US-11-188-298-14827	Sequence 14827, A	513	61	5.1	229	9	US-10-793-626-978	Sequence 978, App
438	62	5.2	516	11	US-11-079-463-6808	Sequence 6808, Ap	514	61	5.1	223	11	US-11-096-568A-8143	Sequence 8143, Ap
439	62	5.2	550	11	US-11-184-380-14	Sequence 14, Appl	515	61	5.1	226	11	US-11-147-916-2	Sequence 2, Appl1
440	62	5.2	580	11	US-11-072-512-3215	Sequence 3215, Ap	516	61	5.1	226	11	US-11-082-389-76	Sequence 76, Appl
441	62	5.2	610	11	US-11-184-380-3	Sequence 3, Appl1	517	61	5.1	276	11	US-11-098-686-11274	Sequence 11274, A
442	62	5.2	687	11	US-11-072-512-2651	Sequence 2651, Ap	518	61	5.1	1288	11	US-11-096-568A-8142	Sequence 8142, A
443	62	5.2	724	9	US-10-469-469-321	Sequence 321, App	519	61	5.1	336	11	US-11-087-099-954	Sequence 954, App
444	62	5.2	724	9	US-10-469-469-322	Sequence 322, App	520	61	5.1	338	11	US-11-096-568A-8141	Sequence 8141, App
445	62	5.2	775	9	US-10-973-1158-120	Sequence 120, App	521	61	5.1	339	11	US-11-174-816-40	Sequence 40, Appl
446	62	5.2	775	11	US-11-290-153-120	Sequence 120, App	522	61	5.1	339	11	US-11-174-816-55	Sequence 55, Appl
449	62	5.2	170	9	US-10-793-626-1164	Sequence 1164, Ap	523	61	5.1	339	11	US-11-174-816-55	Sequence 55, Appl
450	61.5	5.1	173	11	US-11-096-568A-2190	Sequence 2190, Ap	524	61	5.1	339	11	US-11-174-816-55	Sequence 55, Appl
451	61.5	5.1	215	11	US-11-172-740-2126	Sequence 2126, Ap	525	61	5.1	339	11	US-11-174-816-55	Sequence 55, Appl
452	61.5	5.1	215	11	US-11-172-740-2127	Sequence 2127, Ap	526	61	5.1	339	11	US-11-174-816-55	Sequence 55, Appl
453	61.5	5.1	215	11	US-11-172-740-2127	Sequence 2127, Ap	527	61	5.1	339	11	US-11-174-816-55	Sequence 55, Appl
454	61.5	5.1	215	11	US-11-172-740-2127	Sequence 2127, Ap	528	61	5.1	339	11	US-11-174-816-55	Sequence 55, Appl
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456	61.5	5.1	308	11	US-11-004-399-87	Sequence 87, Appl	530	61	5.1	407	11	US-11-087-099-10201	Sequence 10201, A
457	61.5	5.1	308	11	US-11-004-399-457	Sequence 457, Appl	531	61	5.1	407	11	US-11-079-463-6541	Sequence 6541, A
458	61.5	5.1	308	11	US-11-004-399-3890	Sequence 3890, Ap	532	61	5.1	407	11	US-11-096-568A-24857	Sequence 24857, A
459	61.5	5.1	336	11	US-11-096-568A-32529	Sequence 32529, A	533	61	5.1	407	11	US-11-096-568A-17067	Sequence 17067, A
460	61.5	5.1	336	11	US-11-096-568A-32528	Sequence 32528, A	534	61	5.1	407	11	US-11-096-568A-17067	Sequence 17067, A
461	61.5	5.1	390	11	US-11-079-463-9948	Sequence 9948, Ap	535	61	5.1	407	11	US-11-096-568A-17067	Sequence 17067, A
462	61.5	5.1	391	9	US-10-613-744-13	Sequence 13, Appl	536	61	5.1	407	9	US-10-793-626-2632	Sequence 2632, Ap
463	61.5	5.1	425	11	US-11-096-568A-28705	Sequence 28705, A	537	61	5.1	407	9	US-11-188-298-959	Sequence 959, App
464	61.5	5.1	463	9	US-10-510-386-186	Sequence 186, App	538	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
465	61.5	5.1	468	11	US-11-188-298-11107	Sequence 11107, A	539	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
466	61.5	5.1	469	11	US-11-087-099-4007	Sequence 4007, Ap	540	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
467	61.5	5.1	490	11	US-11-068-859-13	Sequence 13, Appl	541	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
468	61.5	5.1	490	11	US-11-068-859-17	Sequence 17, Appl	542	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
469	61.5	5.1	490	11	US-11-068-859-51	Sequence 51, Appl	543	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
470	61.5	5.1	490	11	US-11-068-859-53	Sequence 53, Appl	544	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
471	61.5	5.1	490	11	US-11-068-859-55	Sequence 55, Appl	545	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
472	61.5	5.1	490	11	US-11-068-859-57	Sequence 57, Appl	546	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
473	61.5	5.1	490	11	US-11-068-859-59	Sequence 59, Appl	547	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
474	61.5	5.1	490	11	US-11-068-859-61	Sequence 61, Appl	548	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
475	61.5	5.1	490	11	US-11-068-859-63	Sequence 63, Appl	549	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
476	61.5	5.1	490	11	US-11-068-859-65	Sequence 65, Appl	550	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
477	61.5	5.1	490	11	US-11-068-859-67	Sequence 67, Appl	551	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
478	61.5	5.1	490	11	US-11-068-859-69	Sequence 69, Appl	552	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A
479	61.5	5.1	490	11	US-11-068-859-71	Sequence 71, Appl	553	61	5.1	504	11	US-11-096-568A-17069	Sequence 17069, A

553	61	5.1	704	9	US-10-055-877-113	Sequence 113, App	629	60.5	5.1	825	9	US-10-453-372-644	Sequence 644, App
554	61	5.1	712	11	US-11-096-568A-24855	Sequence 24855, A	630	60.5	5.1	834	9	US-10-453-372-658	Sequence 658, App
555	61	5.1	716	9	US-10-506-454-1056	Sequence 1056, App	631	60.5	5.1	847	9	US-10-453-372-654	Sequence 654, App
556	61	5.1	743	9	US-10-055-877-109	Sequence 109, App	632	60.5	5.1	857	9	US-10-453-372-652	Sequence 652, App
557	61	5.1	774	11	US-11-072-512-2554	Sequence 2554, Ap	633	60.5	5.1	905	9	US-10-453-372-638	Sequence 638, App
558	61	5.1	923	11	US-11-188-298-4931	Sequence 4931, Ap	634	60.5	5.1	905	9	US-10-453-372-662	Sequence 662, App
559	61	5.1	1928	9	US-10-480-330-30	Sequence 30, App1	635	60.5	5.1	905	9	US-10-453-372-663	Sequence 663, App
560	61	5.1	1966	9	US-10-480-330-2	Sequence 2, App11	636	60.5	5.1	963	9	US-10-453-372-660	Sequence 660, App
561	61	5.1	1966	9	US-10-480-330-6	Sequence 6, App11	637	60.5	5.1	963	9	US-10-453-372-660	Sequence 660, App
562	61	5.1	1966	9	US-10-480-330-8	Sequence 8, App11	638	60.5	5.1	1012	9	US-10-453-372-626	Sequence 646, App
563	61	5.1	1966	9	US-10-480-330-10	Sequence 10, App1	639	60.5	5.1	1166	9	US-10-501-035-205	Sequence 205, App
564	61	5.1	1966	9	US-10-480-330-12	Sequence 12, App1	640	60.5	5.1	1207	9	US-10-821-234-1109	Sequence 1109, Ap
565	61	5.1	1966	9	US-10-480-330-14	Sequence 14, App1	641	60.5	5.1	1230	9	US-10-501-035-260	Sequence 260, App
566	61	5.1	1966	9	US-10-480-330-16	Sequence 16, App1	642	60.5	5.1	1932	8	US-10-511-937-2561	Sequence 2561, Ap
567	61	5.1	1966	9	US-10-480-330-18	Sequence 18, App1	643	60	5.0	179	11	US-11-264-096-2103	Sequence 2103, Ap
568	61	5.1	1966	9	US-10-480-330-20	Sequence 20, App1	644	60	5.0	204	9	US-10-793-826-3240	Sequence 3240, Ap
569	61	5.1	1966	9	US-10-480-330-22	Sequence 22, App1	645	60	5.0	247	11	US-11-188-298-461	Sequence 461, App
570	61	5.1	1966	9	US-10-480-330-24	Sequence 24, App1	646	60	5.0	254	11	US-11-188-298-12023	Sequence 12023, A
571	61	5.1	1966	9	US-10-480-330-26	Sequence 26, App1	647	60	5.0	278	11	US-11-098-686-10324	Sequence 10324, A
572	61	5.1	1966	9	US-10-480-330-28	Sequence 28, App1	648	60	5.0	287	11	US-11-087-099-6895	Sequence 6895, Ap
573	61	5.1	3011	9	US-10-985-205-3	Sequence 3, App11	649	60	5.0	290	11	US-11-188-298-18859	Sequence 18859, A
574	61	5.1	3011	10	US-11-140-487A-771	Sequence 771, App	650	60	5.0	292	9	US-10-821-234-966	Sequence 966, App
575	60.5	5.1	191	9	US-10-506-454-695	Sequence 695, App	651	60	5.0	310	9	US-10-485-517-409	Sequence 409, App
576	60.5	5.1	200	11	US-11-167-831-33	Sequence 33, App1	652	60	5.0	333	11	US-11-127-877-57	Sequence 57, App1
577	60.5	5.1	202	11	US-11-098-686-10163	Sequence 10163, A	653	60	5.0	344	11	US-11-172-740-966	Sequence 966, App
578	60.5	5.1	241	11	US-11-096-568A-6296	Sequence 6296, Ap	654	60	5.0	371	11	US-11-087-099-6646	Sequence 6646, Ap
579	60.5	5.1	292	11	US-11-045-004-313	Sequence 313, App	655	60	5.0	403	11	US-11-188-298-623	Sequence 6233, Ap
580	60.5	5.1	294	11	US-11-098-686-10710	Sequence 10710, A	656	60	5.0	411	11	US-11-188-298-2713	Sequence 2713, Ap
581	60.5	5.1	295	11	US-11-188-298-7592	Sequence 7592, Ap	657	60	5.0	462	11	US-11-087-099-11117	Sequence 11117, A
582	60.5	5.1	296	11	US-11-098-686-11275	Sequence 11275, A	658	60	5.0	462	11	US-11-188-298-10265	Sequence 10265, A
583	60.5	5.1	301	9	US-10-973-158B-166	Sequence 166, App	659	60	5.0	468	11	US-11-087-099-9377	Sequence 9377, Ap
584	60.5	5.1	301	9	US-10-973-158B-166	Sequence 166, App	660	60	5.0	468	11	US-11-188-298-8714	Sequence 8714, Ap
587	60.5	5.1	301	11	US-11-290-153-166	Sequence 166, App	661	60	5.0	468	11	US-11-188-298-10370	Sequence 10370, A
588	60.5	5.1	343	11	US-11-045-004-1059	Sequence 1059, Ap	662	60	5.0	469	11	US-11-079-463-5966	Sequence 5966, Ap
589	60.5	5.1	343	11	US-10-793-626-932	Sequence 932, App	663	60	5.0	478	11	US-11-072-512-2898	Sequence 2898, Ap
590	60.5	5.1	355	11	US-11-079-463-6525	Sequence 6525, Ap	664	60	5.0	502	11	US-11-113-424-67	Sequence 67, App1
591	60.5	5.1	359	9	US-10-455-772-1130	Sequence 1130, Ap	665	60	5.0	505	11	US-11-188-298-2050	Sequence 2050, Ap
592	60.5	5.1	359	9	US-10-455-772-1130	Sequence 1130, Ap	666	60	5.0	509	9	US-10-455-772-776	Sequence 776, App
593	60.5	5.1	359	9	US-10-455-772-1130	Sequence 1130, Ap	667	60	5.0	514	11	US-11-188-298-11354	Sequence 11354, A
594	60.5	5.1	365	9	US-10-915-002-237	Sequence 237, App1	668	60	5.0	514	11	US-11-188-298-12674	Sequence 12674, A
595	60.5	5.1	394	11	US-11-043-889-28	Sequence 28, App1	669	60	5.0	519	11	US-11-188-298-18667	Sequence 18667, A
596	60.5	5.1	413	11	US-11-096-568A-25371	Sequence 25371, A	670	60	5.0	519	11	US-10-455-772-780	Sequence 780, App
597	60.5	5.1	421	11	US-11-072-512-3536	Sequence 3536, Ap	671	60	5.0	534	9	US-10-455-772-180	Sequence 205, App
598	60.5	5.1	424	11	US-11-202-731-35	Sequence 35, App1	672	60	5.0	535	9	US-10-506-454-205	Sequence 14, App1
599	60.5	5.1	436	11	US-11-096-568A-9271	Sequence 9271, Ap	673	60	5.0	572	9	US-10-204-639-14	Sequence 18033, A
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601	60.5	5.1	464	11	US-11-096-568A-9270	Sequence 9270, Ap	675	60	5.0	622	11	US-11-188-298-11795	Sequence 21190, A
602	60.5	5.1	471	11	US-11-087-099-9111	Sequence 9111, Ap	676	60	5.0	622	11	US-11-188-298-13119	Sequence 13119, A
603	60.5	5.1	471	11	US-11-188-298-8438	Sequence 8438, Ap	677	60	5.0	622	11	US-11-188-298-21348	Sequence 21348, A
604	60.5	5.1	488	11	US-11-096-568A-25370	Sequence 25370, A	678	60	5.0	624	11	US-11-124-368A-188	Sequence 188, App
605	60.5	5.1	497	11	US-11-087-099-9600	Sequence 9600, Ap	679	60	5.0	624	9	US-10-467-657-1856	Sequence 1856, Ap
606	60.5	5.1	499	9	US-10-793-626-1558	Sequence 1558, Ap	680	60	5.0	724	9	US-10-821-334-1506	Sequence 1506, Ap
607	60.5	5.1	512	11	US-11-096-568A-9269	Sequence 9269, Ap	681	60	5.0	741	11	US-11-188-298-8040	Sequence 8040, Ap
608	60.5	5.1	513	11	US-11-188-298-2716	Sequence 2716, Ap	682	60	5.0	858	9	US-10-995-561-874	Sequence 874, App
609	60.5	5.1	515	9	US-10-055-877-60	Sequence 60, App1	683	60	5.0	858	9	US-10-995-561-875	Sequence 875, App
610	60.5	5.1	516	9	US-10-506-513-2	Sequence 2, App11	684	60	5.0	859	9	US-11-188-298-20296	Sequence 20296, A
611	60.5	5.1	519	11	US-11-087-099-9634	Sequence 9634, Ap	685	60	5.0	869	11	US-11-124-368A-189	Sequence 189, App
612	60.5	5.1	519	11	US-11-096-568A-25369	Sequence 25369, A	686	60	5.0	1068	11	US-11-124-368A-189	Sequence 19455, A
613	60.5	5.1	537	11	US-11-087-099-6132	Sequence 6132, Ap	687	60	5.0	1105	11	US-11-188-298-19455	Sequence 2582, Ap
614	60.5	5.1	537	11	US-11-188-298-16625	Sequence 16625, A	688	59.5	5.0	119	11	US-11-045-004-2562	Sequence 21190, A
615	60.5	5.1	580	11	US-11-087-099-11495	Sequence 11495, A	689	59.5	5.0	140	11	US-11-096-568A-21190	Sequence 21189, A
616	60.5	5.1	580	11	US-11-188-298-21658	Sequence 21658, A	690	59.5	5.0	149	11	US-11-096-568A-21189	Sequence 21189, A
617	60.5	5.1	586	11	US-11-096-568A-9268	Sequence 9268, Ap	691	59.5	5.0	152	11	US-11-079-463-7481	Sequence 7481, Ap
618	60.5	5.1	598	11	US-11-188-298-20619	Sequence 20619, A	692	59.5	5.0	199	11	US-11-155-888-3	Sequence 37, App1
619	60.5	5.1	608	9	US-10-763-712A-16	Sequence 16, App1	693	59.5	5.0	223	11	US-11-155-888-3	Sequence 37, App1
620	60.5	5.1	608	9	US-10-763-712A-90	Sequence 90, App1	694	59.5	5.0	246	11	US-11-264-096-701	Sequence 701, App
621	60.5	5.1	627	11	US-11-188-298-17226	Sequence 17226, A	695	59.5	5.0	247	9	US-10-519-238-1	Sequence 1, App11
622	60.5	5.1	661	9	US-10-453-372-642	Sequence 642, App	696	59.5	5.0	251	9	US-10-519-238-6	Sequence 6, App11
623	60.5	5.1	695	9	US-10-453-372-648	Sequence 648, App	701	59.5	5.0	281	11	US-11-079-463-6581	Sequence 6581, App
624	60.5	5.1	700	9	US-10-995-561-922	Sequence 922, App	702	59.5	5.0	285	11	US-11-096-568A-29502	Sequence 29502, A
625	60.5	5.1	700	9	US-10-995-561-924	Sequence 924, App	703	59.5	5.0	292	11	US-11-172-740-2142	Sequence 2142, Ap
626	60.5	5.1	793	8	US-10-511-937-2614	Sequence 2614, Ap	704	59.5	5.0	307	11	US-11-096-568A-29501	Sequence 29501, A
627	60.5	5.1	793	9	US-10-995-561-925	Sequence 925, App	705	59.5	5.0	312	11	US-11-072-512-2478	Sequence 2478, Ap
628	60.5	5.1	804	9	US-10-453-372-650	Sequence 650, App	706	59.5	5.0	335	11	US-11-188-298-119637	Sequence 19637, A

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709	59.5	5.0	359	9	US-10-506-454-749	Sequence 749, App
710	59.5	5.0	426	11	US-11-096-568A-28439	Sequence 28439, A
711	59.5	5.0	445	9	US-10-793-626-2644	Sequence 2644, Ap
712	59.5	5.0	468	11	US-11-096-568A-34434	Sequence 34434, A
713	59.5	5.0	468	11	US-11-188-298-10510	Sequence 10510, A
714	59.5	5.0	470	11	US-11-096-568A-34433	Sequence 34433, A
715	59.5	5.0	471	11	US-11-087-099-5063	Sequence 5063, Ap
716	59.5	5.0	471	11	US-11-188-298-5678	Sequence 15678, A
717	59.5	5.0	472	11	US-11-096-568A-28438	Sequence 28438, A
718	59.5	5.0	481	11	US-11-188-298-2355	Sequence 2355, Ap
719	59.5	5.0	484	11	US-11-087-099-11511	Sequence 11511, A
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721	59.5	5.0	508	11	US-11-079-463-6229	Sequence 6229, Ap
722	59.5	5.0	511	11	US-11-087-099-7458	Sequence 7458, Ap
723	59.5	5.0	534	11	US-11-188-298-22533	Sequence 22533, A
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726	59.5	5.0	583	11	US-11-188-298-15854	Sequence 15854, A
727	59.5	5.0	657	11	US-11-080-991-48	Sequence 48, Appl
728	59.5	5.0	693	11	US-11-188-298-13968	Sequence 13968, A
729	59.5	5.0	730	11	US-11-096-568A-28437	Sequence 28437, A
730	59.5	5.0	736	11	US-11-087-099-8431	Sequence 8431, Ap
731	59.5	5.0	835	9	US-10-501-039-4	Sequence 4, Appl1
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733	59.5	5.0	865	11	US-11-045-004-2077	Sequence 2077, Ap
734	59.5	5.0	1052	9	US-10-467-657-3992	Sequence 3992, Ap
735	59.5	5.0	1152	11	US-11-024-959-454	Sequence 454, App
736	59.5	5.0	1234	8	US-10-505-928-654	Sequence 654, App
737	59.5	5.0	1244	11	US-11-087-099-9112	Sequence 9112, Ap
738	59.5	5.0	2144	11	US-11-043-889-2	Sequence 2, Appl1
739	59	4.9	167	11	US-11-096-568A-8204	Sequence 8204, Ap
740	59	4.9	173	11	US-11-096-568A-8203	Sequence 8203, Ap
741	59	4.9	177	9	US-10-507-355-4	Sequence 4, Appl1
742	59	4.9	177	11	US-11-087-099-6795	Sequence 375, App
743	59	4.9	181	11	US-11-087-099-6799	Sequence 6799, App
744	59	4.9	184	9	US-10-507-355-7	Sequence 7, Appl1
745	59	4.9	184	11	US-11-096-568A-8202	Sequence 8202, Ap
746	59	4.9	188	11	US-11-096-568A-15158	Sequence 15158, A
747	59	4.9	203	11	US-11-045-004-1927	Sequence 1927, Ap
748	59	4.9	213	11	US-11-096-568A-15157	Sequence 15157, A
749	59	4.9	261	11	US-11-188-298-17162	Sequence 17162, A
750	59	4.9	274	11	US-11-087-099-7024	Sequence 7024, Ap
751	59	4.9	277	11	US-11-146-328-68	Sequence 68, Appl
752	59	4.9	286	11	US-11-082-389-196	Sequence 196, App
753	59	4.9	286	11	US-11-240-769-96	Sequence 96, Appl
754	59	4.9	297	11	US-11-188-298-4712	Sequence 4712, Ap
755	59	4.9	298	11	US-11-264-096-2051	Sequence 2051, Ap
756	59	4.9	304	9	US-10-055-877-173	Sequence 173, App
757	59	4.9	306	11	US-11-188-298-9705	Sequence 9705, Ap
758	59	4.9	332	9	US-10-784-004-359	Sequence 359, App
759	59	4.9	332	9	US-10-784-004-360	Sequence 360, App
760	59	4.9	332	9	US-10-784-004-448	Sequence 448, App
761	59	4.9	343	11	US-11-188-298-16179	Sequence 16179, A
762	59	4.9	344	11	US-11-055-822-516	Sequence 516, App
763	59	4.9	344	11	US-11-188-298-2779	Sequence 2779, Ap
764	59	4.9	347	11	US-11-174-816-42	Sequence 42, Appl1
765	59	4.9	347	11	US-11-174-819-9	Sequence 9, Appl1
766	59	4.9	347	11	US-11-079-463-6856	Sequence 6856, Ap
767	59	4.9	358	9	US-10-467-657-6970	Sequence 6970, Ap
768	59	4.9	376	9	US-10-793-626-490	Sequence 490, App
769	59	4.9	376	9	US-10-793-626-2260	Sequence 2260, Ap
770	59	4.9	395	9	US-10-467-657-1950	Sequence 1950, Ap
771	59	4.9	400	11	US-11-079-463-7215	Sequence 7215, Ap
772	59	4.9	430	11	US-10-467-657-3024	Sequence 3024, Ap
773	59	4.9	430	11	US-11-188-298-7677	Sequence 7677, Ap
774	59	4.9	435	9	US-10-467-657-318	Sequence 318, App
775	59	4.9	462	11	US-11-087-099-8426	Sequence 8426, Ap
776	59	4.9	462	11	US-11-188-298-18809	Sequence 18809, A
777	59	4.9	467	11	US-11-087-099-9910	Sequence 9910, Ap
778	59	4.9	467	11	US-11-087-099-10123	Sequence 10123, A
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780	59	4.9	780	11	US-11-188-298-20347	Sequence 20347, A
781	59	4.9	781	11	US-11-188-298-2971	Sequence 2971, Ap
782	59	4.9	782	9	US-10-745-586-132	Sequence 132, App
783	59	4.9	783	11	US-11-087-099-9913	Sequence 9913, Ap
784	59	4.9	784	11	US-11-188-298-19672	Sequence 19672, A
785	59	4.9	785	11	US-11-045-004-2793	Sequence 2793, Ap
786	59	4.9	786	11	US-11-113-424-65	Sequence 65, Appl
787	59	4.9	787	11	US-11-113-424-66	Sequence 66, Appl
788	59	4.9	788	11	US-11-188-298-20558	Sequence 20558, A
789	59	4.9	789	11	US-11-188-298-2602	Sequence 2602, Ap
790	59	4.9	790	11	US-11-188-298-16525	Sequence 16525, A
791	59	4.9	791	11	US-11-188-298-15517	Sequence 15517, A
792	59	4.9	792	11	US-11-096-568A-29028	Sequence 29028, A
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794	59	4.9	794	11	US-11-068-859-41	Sequence 41, Appl
795	59	4.9	795	11	US-11-068-859-43	Sequence 43, Appl
796	59	4.9	796	11	US-11-068-859-45	Sequence 45, Appl
797	59	4.9	797	11	US-11-068-859-47	Sequence 47, Appl
798	59	4.9	798	11	US-11-068-859-49	Sequence 49, Appl
799	59	4.9	799	11	US-11-068-859-82	Sequence 82, Appl
800	59	4.9	800	11	US-11-068-859-86	Sequence 86, Appl
801	59	4.9	801	11	US-11-068-859-184	Sequence 184, App
802	59	4.9	802	11	US-11-068-859-186	Sequence 186, App
803	59	4.9	803	11	US-11-068-859-197	Sequence 197, App
804	59	4.9	804	11	US-11-096-568A-25027	Sequence 25027, A
805	59	4.9	805	11	US-11-188-298-20578	Sequence 20578, A
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807	59	4.9	807	11	US-11-087-099-6185	Sequence 6185, Ap
808	59	4.9	808	11	US-11-096-568A-20823	Sequence 20823, Ap
809	59	4.9	809	11	US-11-188-298-1742	Sequence 1742, Ap
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812	59	4.9	812	9	US-10-770-726-49	Sequence 49, Appl
813	59	4.9	813	9	US-10-912-580-6	Sequence 6, Appl1
814	59	4.9	814	9	US-10-912-581-1	Sequence 1, Appl1
815	59	4.9	815	8	US-10-511-937-2573	Sequence 2573, Ap
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817	59	4.9	817	11	US-11-096-568A-27722	Sequence 27722, A
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819	59	4.9	819	11	US-11-072-512-2933	Sequence 2933, Ap
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821	59	4.9	821	9	US-10-501-035-319	Sequence 319, App
822	59	4.9	822	11	US-11-096-568A-32051	Sequence 32051, A
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827	59	4.9	827	11	US-10-488-015-12	Sequence 12, Appl
828	58.5	4.9	828	11	US-11-096-568A-11788	Sequence 11788, A
829	58.5	4.9	829	11	US-11-096-568A-11787	Sequence 11787, A
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842	58.5	4.9	842	11	US-11-264-096-1911	Sequence 1911, Ap
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845	58.5	4.9	845	11	US-11-096-568A-23663	Sequence 23663, A
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851	58.5	4.9	851	11	US-11-188-298-12614	Sequence 12614, A
852	58.5	4.9	852	11	US-11-096-568A-23661	Sequence 23661, A



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857	58.5	4.9	429	11	US-11-188-298-21270	Sequence 21270, A	936	58	4.9	376	11	US-11-096-568A-6122	Sequence 6122, Ap
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865	58.5	4.9	445	11	US-11-103-195-32	Sequence 32, Appl	938	58	4.9	391	11	US-11-096-568A-23912	Sequence 23912, A
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867	58.5	4.9	464	11	US-11-087-099-1003	Sequence 1003, Ap	940	58	4.9	394	11	US-11-224-260-5	Sequence 5, Appl1
868	58.5	4.9	466	11	US-11-045-004-104	Sequence 104, App	941	58	4.9	409	11	US-11-188-298-3316	Sequence 3216, Ap
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871	58.5	4.9	487	11	US-11-241-631-14	Sequence 14, Appl	944	58	4.9	423	11	US-11-087-099-7925	Sequence 7925, Ap
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875	58.5	4.9	512	9	US-11-096-568A-19124	Sequence 19124, A	948	58	4.9	426	11	US-11-188-298-13376	Sequence 13376, A
876	58.5	4.9	513	9	US-10-485-517-233	Sequence 233, App	949	58	4.9	439	11	US-11-087-099-739	Sequence 739, App
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886	58.5	4.9	648	9	US-10-330-773-825	Sequence 825, App	959	58	4.9	571	11	US-11-188-298-297	Sequence 2675, Ap
887	58.5	4.9	659	11	US-11-045-004-2524	Sequence 2524, Ap	960	58	4.9	566	11	US-11-072-512-2675	Sequence 4, Appl1
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889	58.5	4.9	733	9	US-10-469-469-323	Sequence 323, App	962	58	4.9	641	11	US-11-062-225-1	Sequence 11264, A
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891	58.5	4.9	885	11	US-11-096-568A-30498	Sequence 30498, A	964	58	4.9	670	11	US-11-188-298-15016	Sequence 15016, A
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893	58.5	4.9	1043	11	US-11-079-463-9606	Sequence 9606, Ap	966	58	4.9	718	8	US-10-511-937-2939	Sequence 2939, Appl
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897	58.5	4.9	2444	11	US-11-188-298-17072	Sequence 17072, A	970	58	4.9	923	11	US-11-087-099-4257	Sequence 7810, Ap
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907	58	4.9	222	11	US-11-264-096-1491	Sequence 1491, Ap	980	58	4.9	1163	11	US-11-044-899-30	Sequence 30, Appl
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911	58	4.9	250	11	US-11-096-568A-12005	Sequence 12005, A	984	57.5	4.8	142	11	US-11-072-175-162	Sequence 162, App
912	58	4.9	254	11	US-11-036-568A-15699	Sequence 15699, A	985	57.5	4.8	142	8	US-10-505-928-169	Sequence 169, App
913	58	4.9	254	11	US-11-096-568A-18368	Sequence 18368, A	986	57.5	4.8	167	9	US-10-821-324-1496	Sequence 1496, Ap
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915	58	4.9	281	11	US-11-082-389-304	Sequence 304, App	988	57.5	4.8	167	9	US-10-506-454-1340	Sequence 1440, Ap
916	58	4.9	291	11	US-11-096-568A-17527	Sequence 17527, A	989	57.5	4.8	173	9	US-10-506-454-176	Sequence 255, App
917	58	4.9	292	11	US-11-045-004-669	Sequence 669, App	990	57.5	4.8	313	11	US-10-524-647-80	Sequence 476, App
918	58	4.9	322	11	US-11-087-099-11014	Sequence 11014, A	991	57.5	4.8	313	11	US-11-188-298-10140	Sequence 10140, A
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920	58	4.9	332	11	US-11-188-298-9437	Sequence 9437, Ap	1006	57.5	4.8	324	11	US-11-188-298-824	Sequence 824, App
921	58	4.9	335	11	US-11-188-298-2295	Sequence 2295, A	1007	57.5	4.8	324	11	US-11-188-298-6472	Sequence 6472, Ap
922	58	4.9	337	11	US-11-079-463-10139	Sequence 10139, A	1008	57.5	4.8	326	11	US-11-188-298-6472	Sequence 239, App
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925	58	4.9	351	11	US-11-174-816-5	Sequence 5, Appl1	1012	57.5	4.8	329	9	US-10-524-647-23	Sequence 23, Appl
926	58	4.9	351	11	US-11-174-819-68	Sequence 68, Appl	1013	57.5	4.8	341	9	US-10-524-647-27	Sequence 27, Appl
927	58	4.9	352	11	US-11-188-298-4433	Sequence 4433, Ap	1014	57.5	4.8	341	9	US-10-524-647-27	Sequence 27, Appl
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930	58	4.9	361	9	US-10-965-103-29	Sequence 29, Appl1	1017	57.5	4.8	353	11	US-11-096-568A-9003	Sequence 9003, Ap
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1023	57.5	4.8	373	11	US-11-044-051-105	Sequence 105, App	1104	57	4.8	246	11	US-11-188-298-8189	Sequence 8189, Ap
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1035	57.5	4.8	408	11	US-11-096-568A-29868	Sequence 29868, A	1116	57	4.8	314	9	US-10-455-772-380	Sequence 380, App
1036	57.5	4.8	417	11	US-11-188-298-8031	Sequence 8031, Ap	1117	57	4.8	317	11	US-11-087-059-9345	Sequence 9345, App
1037	57.5	4.8	418	11	US-11-096-568A-25551	Sequence 25551, A	1118	57	4.8	318	11	US-11-188-298-13758	Sequence 13758, A
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1046	57.5	4.8	519	11	US-11-079-463-9938	Sequence 9938, Ap	1127	57	4.8	370	11	US-11-098-686-10292	Sequence 10292, A
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1061	57.5	4.8	557	11	US-11-096-568A-28054	Sequence 28054, A	1138	57	4.8	430	11	US-11-126-313-36	Sequence 36, Appl
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1065	57.5	4.8	605	11	US-11-290-153-160	Sequence 153, Ap	1141	57	4.8	444	11	US-11-068-859-88	Sequence 88, Appl
1068	57.5	4.8	605	11	US-11-264-096-2237	Sequence 2237, Ap	1142	57	4.8	444	11	US-11-068-859-89	Sequence 89, Appl
1069	57.5	4.8	636	11	US-11-072-512-2225	Sequence 2225, Ap	1143	57	4.8	444	11	US-11-068-859-90	Sequence 90, Appl
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1071	57.5	4.8	727	11	US-11-210-316-8	Sequence 8, Appl	1145	57	4.8	444	11	US-11-068-859-92	Sequence 92, Appl
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1090	57.5	4.8	3674	11	US-11-000-463-454	Sequence 454, App	1164	57	4.8	454	11	US-11-068-859-85	Sequence 85, Appl
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1095	57	4.8	135	11	US-11-098-686-10095	Sequence 10095, A	1169	57	4.8	454	11	US-11-068-859-166	Sequence 166, App
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1098	57	4.8	174	11	US-11-079-463-10145	Sequence 10145, A	1172	57	4.8	454	11	US-11-068-859-173	Sequence 173, App

1173	57	4.8	454	11	US-11-068-859-179	Sequence 179, App	1246	56.5	4.7	269	9	US-10-986-405-201	Sequence 201, App
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1176	57	4.8	454	11	US-11-068-859-193	Sequence 193, App	1249	56.5	4.7	280	11	US-11-079-463-6326	Sequence 6326, App
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1189	57	4.8	522	9	US-10-455-772-1002	Sequence 1002, App	1262	56.5	4.7	329	9	US-10-524-972-2	Sequence 2, App
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1194	57	4.8	553	11	US-11-188-298-16884	Sequence 16884, A	1267	56.5	4.7	347	11	US-11-174-816-57	Sequence 57, App
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1212	57	4.8	834	9	US-10-928-446A-196	Sequence 196, App	1285	56.5	4.7	433	11	US-11-188-298-14554	Sequence 14554, A
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1242	56.5	4.7	183	11	US-11-188-298-8788	Sequence 8788, App	1315	56.5	4.7	567	11	US-11-096-568A-9801	Sequence 9801, App
1243	56.5	4.7	200	11	US-11-167-831-35	Sequence 35, App	1316	56.5	4.7	580	11	US-11-188-298-945	Sequence 945, App
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1325	56.5	4.7	662	11	US-11-188-298-13798	Sequence 13798, A	1412	56	4.7	430	11	US-11-199-821-2	Sequence 2, Appl
1326	56.5	4.7	670	11	US-11-079-463-5350	Sequence 5350, Ap	1413	56	4.7	433	11	US-11-087-099-9359	Sequence 9359, Ap
1327	56.5	4.7	674	9	US-10-467-657-6812	Sequence 6812, Ap	1414	56	4.7	443	11	US-11-087-059-91	Sequence 91, Appl
1328	56.5	4.7	730	9	US-10-703-7998-218	Sequence 218, App	1415	56	4.7	445	11	US-11-087-099-11856	Sequence 11856, A
1329	56.5	4.7	730	11	US-11-082-389-358	Sequence 358, App	1416	56	4.7	458	11	US-11-087-099-5424	Sequence 5424, Ap
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1333	56.5	4.7	817	11	US-11-072-512-2301	Sequence 2301, Ap	1420	56	4.7	475	11	US-11-087-099-4508	Sequence 4508, Ap
1334	56.5	4.7	852	11	US-11-072-512-3646	Sequence 3646, Ap	1421	56	4.7	475	11	US-11-096-568A-5504	Sequence 5504, Ap
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1337	56.5	4.7	885	11	US-11-188-298-13076	Sequence 13076, A	1424	56	4.7	489	11	US-11-087-099-4454	Sequence 4454, Ap
1338	56.5	4.7	1066	11	US-11-045-004-1581	Sequence 1581, Ap	1425	56	4.7	489	11	US-11-087-099-11342	Sequence 11342, A
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1344	56	4.7	153	11	US-11-096-568A-9576	Sequence 9576, Ap	1431	56	4.7	503	11	US-11-096-568A-28202	Sequence 28202, A
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1369	56	4.7	291	11	US-11-188-298-342	Sequence 342, App	1456	56	4.7	590	11	US-11-188-298-6096	Sequence 6096, Ap
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1371	56	4.7	303	11	US-11-188-298-18841	Sequence 18841, A	1458	56	4.7	594	11	US-11-188-298-9040	Sequence 9040, Ap
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1376	56	4.7	322	9	US-10-487-767-3	Sequence 1646, Ap	1463	56	4.7	595	9	US-10-455-772-226	Sequence 226, App
1377	56	4.7	332	9	US-10-487-767-3	Sequence 25716, A	1464	56	4.7	595	9	US-10-455-772-228	Sequence 228, App
1378	56	4.7	334	11	US-11-096-568A-25716	Sequence 25716, A	1465	56	4.7	595	9	US-10-455-772-230	Sequence 232, App
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1385	56	4.7	373	11	US-11-218-281-1	Sequence 1, Appl	1472	56	4.7	604	11	US-10-533-066-1	Sequence 1, Appl
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1387	56	4.7	373	11	US-11-087-099-11642	Sequence 11642, A	1474	56	4.7	604	11	US-10-784-004-412	Sequence 412, App
1388	56	4.7	373	11	US-11-188-298-21819	Sequence 21819, A	1475	56	4.7	604	11	US-11-079-463-9524	Sequence 9524, Ap
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1482	56	4.7	1972	11	US-11-124-367A-446	Sequence 446, App
1483	56	4.7	2505	11	US-11-126-313-33	Sequence 33, Appl
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1485	55.5	4.6	102	11	US-11-199-739-26	Sequence 26, Appl
1486	55.5	4.6	135	11	US-11-087-099-7114	Sequence 7114, Ap
1487	55.5	4.6	139	11	US-11-172-740-625	Sequence 625, App
1488	55.5	4.6	149	11	US-11-096-568A-4066	Sequence 4066, Ap
1489	55.5	4.6	180	11	US-11-165-697-47	Sequence 47, Appl
1490	55.5	4.6	187	11	US-11-087-099-9846	Sequence 9846, Ap
1491	53.5	4.6	193	11	US-11-096-568A-21794	Sequence 21794, A
1492	55.5	4.6	197	9	US-10-714-887-134	Sequence 134, App
1493	55.5	4.6	230	11	US-11-087-099-10122	Sequence 10122, A
1494	55.5	4.6	234	11	US-11-096-568A-21717	Sequence 21717, A
1495	55.5	4.6	236	11	US-11-098-686-11423	Sequence 11423, A
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OM protein - protein search, using sw model

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(without alignments)  
549.140 Million cell updates/sec

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Perfect score: 1195  
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Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	664	55.6	445	2 I38027	MLN 64 protein - h
2	204	17.1	478	2 T16170	hypothetical prote
3	102.5	8.6	348	2 H90281	hypothetical prote
4	93.5	7.8	424	2 D75080	glucose-1-phosphat
5	90	7.5	1911	2 T43048	calcium channel al
6	86.5	7.2	767	2 T21969	hypothetical prote
7	85.5	7.2	396	2 B81299	probable molybdopt
8	85.5	7.2	438	2 A57219	Batten disease-rel
9	85	7.1	448	2 G70172	conserved hypochet
10	84.5	7.1	471	2 A41680	integral membrane
11	83.5	7.0	352	2 H97002	probable integral
12	83	6.9	291	2 AE0302	sugar ABC transpor
13	83	6.9	590	1 S34960	NADH2 dehydrogenas
14	82.5	6.9	186	2 B29835	Tras protein - Esc
15	82.5	6.9	239	1 C64237	hypothetical prote
16	82.5	6.9	341	2 S51265	probable N-acetylgl
17	82.5	6.9	406	2 T43120	conserved hypochet
18	82.5	6.9	891	2 T37397	major core protein
19	82	6.9	589	2 T52070	RNAI protein homol
20	82	6.9	589	2 A36983	RNAI homolog fup1
21	82	6.9	1466	2 T30566	ATP-binding casest
22	81	6.8	385	2 B84447	hypothetical prote
23	81	6.8	329	2 T23150	hypothetical prote
24	81	6.8	532	2 S46831	probable membrane
25	80.5	6.7	156	2 I84498	melatonin receptor
26	80.5	6.7	322	2 T45568	hypothetical prote
27	80.5	6.7	396	2 T50229	probable transmemb
28	80.5	6.7	417	2 C44038	tryptophan permeas
29	80.5	6.7	463	2 AE1155	amino acid transpo

30	80.5	6.7	536	2 A71491	probable integral
31	80.5	6.7	644	2 S63056	probable membrane
32	80.5	6.7	738	2 S10659	membrane protein t
33	80.5	6.7	891	1 MWV235	major core protein
34	80.5	6.7	891	1 MWV23W	major core protein
35	80.5	6.7	1780	2 AB5045	probable glucan sy
36	80	6.7	103	2 G75513	conserved hypochet
37	80	6.7	290	2 D89898	hypothetical prote
38	80	6.7	309	2 S59140	RTM protein - yea
39	80	6.7	388	2 H71115	hypothetical prote
40	80	6.7	1339	2 A84683	probable SNF2 subu
41	79.5	6.7	463	2 AH1513	amino acid transpo
42	79.5	6.7	491	1 EDBE1C	immediate-early pr
43	78.5	6.6	239	2 T37812	hypothetical prote
44	78.5	6.6	269	2 AF1532	spermidine/putresc
45	78.5	6.6	358	2 F64136	rnfD protein homol
46	78.5	6.6	471	2 S11280	serotonin receptor
47	78.5	6.6	678	2 S44925	IB3/5-polypeptide
48	78	6.5	245	2 JC5346	cdd2 protein - Clo
49	78	6.5	259	2 F83825	hypothetical prote
50	78	6.5	382	2 E97157	stage III sporulat
51	78	6.5	471	2 B64099	undecaprenyl-phosp
52	78	6.5	1297	2 T39287	hypothetical prote
53	78	6.5	2136	2 A05037	hypothetical prote
54	77.5	6.5	269	2 AH1175	spermidine/putresc
55	77.5	6.5	327	2 AE0461	probable membrane
56	77.5	6.5	327	2 F82904	conserved hypochet
57	77.5	6.5	328	2 F84130	ABC transporter (p
58	77.5	6.5	338	2 T39159	hypothetical prote
59	77.5	6.5	440	2 T11319	NADH2 dehydrogenas
60	77.5	6.5	491	2 B69499	sodium- and chlori
61	77.5	6.5	512	2 AC3399	probable colanic b
62	77.5	6.5	734	1 DER2N5	NADH2 dehydrogenas
63	77.5	6.5	892	2 H72164	hypothetical prote
64	77.5	6.5	892	2 T28552	hypothetical prote
65	77.5	6.5	892	2 B36849	A101 protein - var
66	77.5	6.5	1784	2 T43167	sodium channel pro
67	77	6.4	332	2 T23107	hypothetical prote
68	77	6.4	539	2 C87307	hypothetical prote
69	77	6.4	590	1 Q0UTC5	NADH2 dehydrogenas
70	77	6.4	650	2 A90072	hypothetical prote
71	77	6.4	991	2 T01377	hypothetical prote
72	77	6.4	1025	2 T18376	multidrug resistan
73	77	6.4	1117	2 C85018	hypothetical prote
74	77	6.4	1500	2 G84922	hypothetical prote
75	76.5	6.4	278	2 B85807	probable tail fibe
76	76.5	6.4	282	2 H90958	phage tail protein
77	76.5	6.4	352	2 H95869	probable sugar ABC
78	76.5	6.4	352	2 T25170	hypothetical prote
79	76.5	6.4	352	2 AF0692	probable membrane
80	76.5	6.4	434	2 UC5919	potassium channel
81	76.5	6.4	538	2 E81435	probable iron-upta
82	76.5	6.4	589	2 A71918	probable secretion
83	76.5	6.4	646	2 T41545	hypothetical trans
84	76	6.4	342	2 T11476	NADH2 dehydrogenas
85	76	6.4	402	2 T24184	hypothetical prote
86	76	6.4	669	2 T48466	hypothetical prote
87	76	6.4	1402	2 T24664	hypothetical prote
88	76	6.4	1450	2 JC6139	cystic fibrosis tr
89	75	6.4	1783	2 T37258	probable voltage-d
90	75	6.4	1917	2 C88728	protein C48A7.1 (l
91	75.5	6.3	156	2 I62107	melatonin receptor
92	75.5	6.3	263	2 G95198	hypothetical prote
93	75.5	6.3	263	2 C98065	hypothetical prote
94	75.5	6.3	339	2 E82211	conserved hypochet
95	75.5	6.3	332	2 H64919	probable membrane
96	75.5	6.3	352	2 G85769	hypothetical prote
97	75.5	6.3	352	2 C90921	hypothetical prote
98	75.5	6.3	415	2 F91209	low affinity trypt
99	75.5	6.3	415	2 A86056	low affinity trypt
100	75.5	6.3	415	2 A39412	tryptophan transpo
101	75.5	6.3	471	2 S40689	5-hydroxytryptamin
102	75.5	6.3	498	2 T11039	NADH2 dehydrogenas

103	75.5	6.3	593	2	H64594	multidrug resistan
104	75.5	6.3	708	2	T29669	hypothetical prote
105	75.5	6.3	775	2	T52107	anion channel prote
106	75.5	6.3	1142	2	T39103	probable negative
107	75	6.3	249	2	G64470	sulfate/chitosulat
108	75	6.3	274	2	A82509	probable phosphati
109	75	6.3	430	2	B71163	probable oligopept
110	75	6.3	373	2	A38627	gamma-aminobutyric
111	75	6.3	526	2	T45850	hypothetical prote
112	75	6.3	649	2	C69810	anion-binding prot
113	75	6.3	753	2	H90124	hypothetical prote
114	75	6.3	2248	1	D42088	adenylate cyclase
115	74.5	6.2	276	2	A95881	probable trehalase
116	74.5	6.2	335	2	H72420	oligopeptide ABC t
117	74.5	6.2	355	2	JC4304	orphan G protein-c
118	74.5	6.2	471	2	A34863	serotonin receptor
119	74.5	6.2	473	2	B84143	Na+/H+ antiporter
120	74.5	6.2	500	2	T14826	transcription init
121	74.5	6.2	574	2	T05964	probable low-affin
122	74.5	6.2	618	2	S38004	probable transport
123	74.5	6.2	1808	2	T47792	hypothetical prote
124	74	6.2	231	1	C69540	cobalamin (5'-phos
125	74	6.2	231	1	B69422	quinone-reactive N
126	74	6.2	281	1	S26018	NADH2 dehydrogenas
127	74	6.2	286	2	S73424	spermidine/putresc
128	74	6.2	312	2	C72547	probable aspartate
129	74	6.2	312	2	H86732	hypothetical prote
130	74	6.2	349	2	JC6311	interferon recepto
131	74	6.2	350	2	I38848	Mel-1a melatonin r
132	74	6.2	396	2	H89869	hypothetical prote
133	74	6.2	442	2	C86859	transmembrane effl
134	74	6.2	449	2	S02011	serotonin receptor
135	74	6.2	475	2	T36137	probable amino aci
136	74	6.2	485	2	T24115	hypothetical prote
137	74	6.2	487	1	C71417	cytochrome P450 d1
138	74	6.2	493	2	JC7378	L-lysine 6-aminotr
139	74	6.2	1123	2	T51517	telomerase reverse
140	73.5	6.2	153	2	E95845	conserved hypotet
141	73.5	6.2	192	2	A84727	hypothetical prote
142	73.5	6.2	216	2	G70474	hypothetical prote
143	73.5	6.2	318	2	S76713	hypothetical prote
144	73.5	6.2	338	2	I40448	conserved hypotet
145	73.5	6.2	379	2	S58448	ubiquinol-cytochro
146	73.5	6.2	384	2	AF0636	glucanase biosynthes
147	73.5	6.2	385	1	S01511	ubiquinol-cytochro
148	73.5	6.2	385	2	A69804	ABC transporter (A
149	73.5	6.2	413	2	AD1738	Similar to multidr
150	73.5	6.2	442	2	C96672	hypothetical prote
151	73.5	6.2	491	1	EDBEM5	immediate-early pr
152	73.5	6.2	634	2	F82623	potaesium uptake p
153	73.5	6.2	637	2	H83945	DNA mismatch repai
154	73.5	6.2	640	2	B32935	hypothetical prote
155	73.5	6.2	731	2	T31914	hypothetical prote
156	73.5	6.2	1095	2	E96744	probable oligopept
157	73.5	6.2	1174	2	A39927	RNA-directed RNA p
158	73	6.1	114	2	F71925	cag island protein
159	73	6.1	282	2	S26030	NADH2 dehydrogenas
160	73	6.1	350	2	T15360	hypothetical prote
161	73	6.1	450	1	WZBE64	49.2K membrane pro
162	73	6.1	453	2	T30985	hypothetical prote
163	73	6.1	553	2	A71823	hypothetical prote
164	73	6.1	788	2	G89901	hypothetical prote
165	73	6.1	1075	2	T00258	hypothetical prote
166	73	6.1	1075	2	B96508	hypothetical prote
167	73	6.1	6805	2	S20901	clitin - rabbit (fr
168	72.5	6.1	209	2	S72929	hypothetical prote
169	72.5	6.1	222	2	B85866	probable transport
170	72.5	6.1	222	2	B91032	probable transport
171	72.5	6.1	222	2	H64996	hypothetical prote
172	72.5	6.1	255	2	A60944	ubiquinol-cytochro
173	72.5	6.1	291	2	T02986	chlorophyll a/b-bi
174	72.5	6.1	307	2	A86696	conserved hypotet
175	72.5	6.1	315	2	H96598	protein F20N2.8 [i
176	72.5	6.1	325	2	H86670	hypothetical prote
177	72.5	6.1	336	2	C88951	protein G38C3.2 [i
178	72.5	6.1	389	2	A55493	oxytocin receptor
179	72.5	6.1	428	2	AF0173	probable paraquat-
180	72.5	6.1	499	2	H70453	vinculance factor M
181	72.5	6.1	513	2	S47631	pituitary adenylat
182	72.5	6.1	522	2	T29705	hypothetical prote
183	72.5	6.1	635	2	T23465	hypothetical prote
184	72.5	6.1	718	2	S57913	probable transloac
185	72.5	6.1	749	2	C84508	probable cap-bindi
186	72.5	6.1	1539	2	T30037	hypothetical prote
187	72	6.0	279	2	T21039	hypothetical prote
188	72	6.0	306	2	AB1156	hypothetical prote
189	72	6.0	339	2	G97199	probable permease
190	72	6.0	377	2	T27805	hypothetical prote
191	72	6.0	379	2	T11349	ubiquinol-cytochro
192	72	6.0	415	1	WMAD52	late LI 52K protei
193	72	6.0	415	1	WMAD55	late LI 52K protei
194	72	6.0	453	2	T39155	glycosyl hydrolyase
195	72	6.0	453	2	D89760	conserved hypotet
196	72	6.0	479	2	S64587	hypothetical prote
197	72	6.0	497	2	G96611	probable cytochrom
198	72	6.0	514	2	T15338	hypothetical prote
199	72	6.0	594	2	T42660	hypothetical prote
200	72	6.0	600	2	T39873	probable ethylene
201	72	6.0	630	2	T07966	hypothetical prote
202	72	6.0	1038	2	S37854	DNA-directed DNA p
203	72	6.0	1094	2	S22573	hypothetical prote
204	72	6.0	1113	2	T20140	patched protein -
205	72	6.0	1220	2	T18291	hypothetical prote
206	72	6.0	1275	2	JU0092	trp protein - frui
207	72	6.0	1282	2	T30804	P-glycoprotein 6 -
208	71.5	6.0	210	2	S52050	cytochrome-c oxid
209	71.5	6.0	225	1	MMIH68	E1 membrane glycop
210	71.5	6.0	237	2	H70975	hypothetical prote
211	71.5	6.0	246	2	AG3644	flagellar biosynth
212	71.5	6.0	301	2	F66647	hypothetical prote
213	71.5	6.0	341	2	F90084	hypothetical prote
214	71.5	6.0	345	2	T37066	hypothetical prote
215	71.5	6.0	348	2	D82252	RnfD-related prote
216	71.5	6.0	355	2	AB3516	sensory transducti
217	71.5	6.0	362	2	S48689	prostoglandin E(2)
218	71.5	6.0	366	2	S51280	Ep3-alpha receptor
219	71.5	6.0	366	2	I46469	Mel-1a melatonin r
220	71.5	6.0	381	2	T11776	ubiquinol-cytochro
221	71.5	6.0	383	2	T38194	hypothetical prote
222	71.5	6.0	386	1	S34043	oxytocin receptor
223	71.5	6.0	390	2	S66497	islotocin receptor
224	71.5	6.0	435	2	AD1340	maltodextrin ABC-t
225	71.5	6.0	435	2	AB1711	maltodextrin ABC-t
226	71.5	6.0	471	2	PS0154	125K surface anti
227	71.5	6.0	510	2	T10124	hexose transport p
228	71.5	6.0	524	2	T02499	hypothetical prote
229	71.5	6.0	603	2	H90061	hypothetical prote
230	71.5	6.0	651	2	T46050	hypothetical prote
231	71.5	6.0	669	2	DC4137	bet1 protein homol
232	71.5	6.0	670	2	A49580	mediates transport
233	71.5	6.0	823	2	T34472	hypothetical prote
234	71.5	6.0	1407	2	B42239	adenylate cyclase
235	71.5	6.0	3010	1	S18030	genome polyprotein
236	71	5.9	345	2	H64586	cag pathogenicity
237	71	5.9	345	2	T12372	E1 membrane glycop
238	71	5.9	345	2	T25561	conserved hypotet
239	71	5.9	358	2	AB1355	probable processin
240	71	5.9	390	2	S33443	chlorophyll a/b-bi
241	71	5.9	399	2	T16745	hypothetical prote
242	71	5.9	345	2	T25561	NADH2 dehydrogenas
243	71	5.9	345	2	T25561	hypothetical prote
244	71	5.9	391	2	C90603	hypothetical prote
245	71	5.9	391	2	F86759	hypothetical prote
246	71	5.9	416	2	B87286	3-deoxy-D-manno-oc
247	71	5.9	423	2	AF1335	transcription regu
248	71	5.9	471	2	A43956	serotonin receptor



249	71	5.9	546	2	S48932	hypothetical prote
250	71	5.9	563	2	T38766	probable transcript
251	71	5.9	576	2	T22509	hypothetical prote
252	71	5.9	620	2	A58932	cytochrome C-type
253	71	5.9	676	2	E96725	hypothetical prote
254	71	5.9	788	2	E17813	probable component
255	71	5.9	913	2	T52485	neurofilament prot
256	71	5.9	2437	2	T18482	hypothetical prote
257	70.5	5.9	203	1	T1684	probable bacitraci
258	70.5	5.9	266	2	H98208	probable permease
259	70.5	5.9	266	2	A13077	hypothetical prote
260	70.5	5.9	266	2	T14144	probable receptor-
261	70.5	5.9	279	2	AH2408	permease protein o
262	70.5	5.9	291	2	S22041	hypothetical prote
263	70.5	5.9	340	2	S76294	hypothetical prote
264	70.5	5.9	352	2	B90537	hypothetical prote
265	70.5	5.9	365	2	T18748	prostaglandin recep
266	70.5	5.9	365	2	S51335	prostaglandin E re
267	70.5	5.9	374	2	T18747	prostaglandin recep
268	70.5	5.9	374	2	S51317	prostaglandin E re
269	70.5	5.9	388	2	S51316	prostaglandin E re
270	70.5	5.9	388	2	T18750	prostaglandin recep
271	70.5	5.9	389	2	S71336	mesococin receptor
272	70.5	5.9	390	2	S43375	prostaglandin E re
273	70.5	5.9	390	2	S51313	prostaglandin E re
274	70.5	5.9	393	2	S51318	prostaglandin E re
275	70.5	5.9	423	1	E71065	hypothetical prote
276	70.5	5.9	425	2	S51319	prostaglandin E re
277	70.5	5.9	472	2	AG3600	cellulose synthase
278	70.5	5.9	496	2	B64638	conserved hypothet
279	70.5	5.9	521	2	B64181	probable cytochrom
280	70.5	5.9	548	2	AB1650	conserved hypothet
281	70.5	5.9	556	2	T16790	hypothetical prote
282	70.5	5.9	574	2	S45754	probable membrane
283	70.5	5.9	599	1	P46027	gamma-aminobutyric
284	70.5	5.9	599	1	ACRRTG	gamma-aminobutyric
285	70.5	5.9	766	2	T10566	probable serine/th
286	70.5	5.9	766	2	T48463	hypothetical prote
287	70.5	5.9	1026	2	T18220	chitin synthase (E
288	70.5	5.9	1583	2	F97846	hypothetical prote
289	70.5	5.9	1787	2	T20160	hypothetical prote
290	70.5	5.9	5138	2	B66695	hypothetical prote
291	70	5.9	189	2	T51847	manganese-binding
292	70	5.9	199	2	T08902	manganese-binding
293	70	5.9	213	2	F86310	protein PilJ.8 [lm
294	70	5.9	233	2	T13597	hypothetical prote
295	70	5.9	287	2	T52317	chlorophyll a/b-bi
296	70	5.9	292	2	H64244	H+-transporting tw
297	70	5.9	307	2	E95010	ABC transporter, p
298	70	5.9	307	2	B97882	hypothetical prote
299	70	5.9	330	2	T30981	hypothetical prote
300	70	5.9	333	2	T38974	G protein-coupled
301	70	5.9	371	2	T46421	hypothetical prote
302	70	5.9	388	2	A55597	oxytocin receptor
303	70	5.9	416	2	AB5112	probable ankyrin-r
304	70	5.9	418	2	T08882	proline/betaine tr
305	70	5.9	420	2	E72357	sugar ABC transpor
306	70	5.9	427	2	T01905	hypothetical prote
307	70	5.9	437	2	C91261	glutamate-aspartat
308	70	5.9	437	2	G86101	glutamate-aspartat
309	70	5.9	438	2	AF3215	ABC transporter, m
310	70	5.9	450	2	T42595	envelope protein 5
311	70	5.9	494	2	B89827	hypothetical prote
312	70	5.9	532	2	T49467	related to COP1-in
313	70	5.9	551	2	A87019	probable cytochrom
314	70	5.9	551	2	T27878	hypothetical prote
315	70	5.9	558	2	H72565	hypothetical prote
316	70	5.9	675	2	T23233	hypothetical prote
317	70	5.9	735	2	S46830	urea transport pro
318	70	5.9	963	2	T26022	hypothetical prote
319	70	5.9	1930	2	F86200	protein Fl2X1.17
320	69.5	5.8	133	1	MNIHHC	nonstructural prot
321	69.5	5.8	206	2	S76279	hypothetical prote
322	69.5	5.8	322	2	F70194	hypothetical prote
323	69.5	5.8	323	2	S59388	probable membrane
324	69.5	5.8	324	2	A97736	hypothetical prote
325	69.5	5.8	325	2	G90444	hypothetical prote
326	69.5	5.8	326	2	I58186	probable G protein
327	69.5	5.8	327	2	A53216	prostaglandin E2 r
328	69.5	5.8	328	2	S36766	prostaglandin E re
329	69.5	5.8	329	2	S62758	ubiquinol-cytochro
330	69.5	5.8	330	2	S36765	prostaglandin E re
331	69.5	5.8	331	2	S36767	prostaglandin E re
332	69.5	5.8	332	2	T32561	hypothetical prote
333	69.5	5.8	333	2	AG1208	cell-division prot
334	69.5	5.8	334	2	S51791	Drosophila translo
335	69.5	5.8	335	2	E90986	probable colanic a
336	69.5	5.8	336	2	H85831	probable colanic a
337	69.5	5.8	337	2	G64971	putative colanic a
338	69.5	5.8	338	2	B53216	prostaglandin E2 r
339	69.5	5.8	339	2	S36764	prostaglandin E re
340	69.5	5.8	340	2	G72300	conserved hypothet
341	69.5	5.8	341	2	T44832	probable emulsan r
342	69.5	5.8	342	2	D98003	conserved hypothet
343	69.5	5.8	343	2	T25798	hypothetical prote
344	69.5	5.8	344	2	E82740	C4-dicarboxylate t
345	69.5	5.8	345	2	C86250	hypothetical prote
346	69.5	5.8	346	2	T50054	probable transport
347	69.5	5.8	347	2	E86534	ADP/ATP translocas
348	69.5	5.8	348	2	G86581	integral membrane
349	69.5	5.8	349	2	F72042	integral membrane
350	69.5	5.8	350	2	JW0089	organic cation tra
351	69.5	5.8	351	2	AC2137	ABC transporter AT
352	69.5	5.8	352	2	B96776	hypothetical prote
353	69.5	5.8	353	2	D97337	mismatch repair pr
354	69.5	5.8	354	2	AG1412	DNA polymerase III
355	69.5	5.8	355	2	AF1788	DNA polymerase III
356	69.5	5.8	356	2	S11073	gamma-aminobutyric
357	69.5	5.8	357	2	T31042	hypothetical prote
358	69.5	5.8	358	2	F84525	Mutator-like trans
359	69.5	5.8	359	2	E84463	Mutator-like trans
360	69.5	5.8	360	2	S58824	probable membrane
361	69.5	5.8	361	2	S46633	probable membrane
362	69.5	5.8	362	2	S71363	probable ATP-bindi
363	69.5	5.8	363	2	A59188	ATP-binding cassel
364	69.5	5.8	364	2	JT0382	apolipoprotein B -
365	69.5	5.8	365	2	T46569	apolipoprotein B -
366	69.5	5.8	366	2	T15789	hypothetical prote
367	69.5	5.8	367	2	E83941	hypothetical prote
368	69.5	5.8	368	2	A96998	CDP-diacylglycerid
369	69.5	5.8	369	2	H96934	uncharacterized me
370	69.5	5.8	370	2	G64145	hypothetical prote
371	69.5	5.8	371	2	T07481	hypothetical prote
372	69.5	5.8	372	2	F83805	hypothetical prote
373	69.5	5.8	373	2	C71707	hypothetical prote
374	69.5	5.8	374	2	S72554	melatonin receptor
375	69.5	5.8	375	2	D96002	probable sugar upt
376	69.5	5.8	376	2	T32702	hypothetical prote
377	69.5	5.8	377	2	A99979	hypothetical prote
378	69.5	5.8	378	2	B69436	Leu ribosomal prot
379	69.5	5.8	379	2	ADH154	hypothetical prote
380	69.5	5.8	380	2	AD0273	probable integral
381	69.5	5.8	381	2	S58447	ubiquinol-cytochro
382	69.5	5.8	382	2	A13175	conserved hypothet
383	69.5	5.8	383	2	D71424	O-antigen polymera
384	69.5	5.8	384	2	T69644	MNDH2 dehydrogenas
385	69.5	5.8	385	2	T11268	glutamate-aspartat
386	69.5	5.8	386	2	A42384	hypothetical prote
387	69.5	5.8	387	2	T19512	transposase - Bacti
388	69.5	5.8	388	2	S25821	hypothetical prote
389	69.5	5.8	389	2	T33985	probable thiorodox
390	69.5	5.8	390	2	B96804	MNDH2 dehydrogenas
391	69.5	5.8	391	2	T11916	hypothetical prote
392	69.5	5.8	392	2	T24675	cytochrome b homol
393	69.5	5.8	393	2	E70784	inner membrane cop
394	69.5	5.8	394	2	A64100	

395	69	5.8	599	2	G90476	probable Na+/H+ an	468	68	5.7	426	2	C69831	conserved hypochet
396	69	5.8	600	2	T11869	NADH2 dehydrogenas	469	68	5.7	464	2	C70414	NADH2 dehydrogenas
397	69	5.8	637	2	H65592	probable multipep	470	68	5.7	473	2	H71044	hypothetical prote
398	69	5.8	639	2	D84633	hypothetical prote	471	68	5.7	475	2	E83450	cytochrome-c oxida
399	69	5.8	791	2	T12455	potassium channel	472	68	5.7	477	2	H91123	probable oxidoredu
400	69	5.8	802	2	JH0595	hypothetical prote	473	68	5.7	477	2	G85968	probable oxidoredu
401	69	5.8	863	2	H84490	hypothetical prote	474	68	5.7	477	2	C65096	hypothetical 52.1 r
402	69	5.8	933	2	AD3309	hypothetical membr	475	68	5.7	488	2	A53572	prostaglandin E2 r
403	69	5.8	1058	2	T30580	p-type ATPase - sl	476	68	5.7	502	1	I30010	NADH2 dehydrogenas
404	69	5.8	1344	2	T34188	myb-binding protei	477	68	5.7	519	2	T39918	probable acetyl-co
405	69	5.8	1392	2	T01908	hypothetical prote	478	68	5.7	542	2	A69261	probable acid-CoA
406	69	5.8	1515	2	T04204	hypothetical prote	479	68	5.7	542	2	B81910	probable ABC-trans
407	69	5.8	3010	1	A45573	genome polyprotein	480	68	5.7	542	2	E81105	hypothetical prote
408	68.5	5.7	225	2	AE0371	probable carboxype	481	68	5.7	620	2	T19907	probable receptor
409	68.5	5.7	237	2	T25877	hypothetical prote	482	68	5.7	664	2	C84869	hypothetical prote
410	68.5	5.7	238	2	T04280	hypothetical prote	483	68	5.7	718	2	E83718	hypothetical prote
411	68.5	5.7	260	2	H75428	hypothetical prote	484	68	5.7	804	2	T49975	hypothetical prote
412	68.5	5.7	262	2	AG1830	hypothetical prote	485	68	5.7	836	2	T18460	hypothetical prote
413	68.5	5.7	265	2	A13428	O-antigen export s	486	68	5.7	859	2	S69700	hypothetical prote
414	68.5	5.7	285	2	E86835	malose ABC transp	487	68	5.7	871	2	H72597	hypothetical prote
415	68.5	5.7	297	2	S74335	carbon dioxide con	488	68	5.7	1429	2	T19422	hypothetical prote
416	68.5	5.7	304	2	AG3035	hypothetical prote	489	68	5.7	1878	2	E86189	hypothetical prote
417	68.5	5.7	304	2	D98250	probable sugar ABC	490	68	5.7	3010	1	GNMYTC	genome polyprotein
418	68.5	5.7	333	2	AC2129	iron(III) diclirat	491	67.5	5.6	104	2	T36801	hypothetical prote
419	68.5	5.7	339	2	B59105	hypothetical prote	492	67.5	5.6	200	2	H72295	conserved hypochet
420	68.5	5.7	352	2	D72424	oligopeptide ABC t	493	67.5	5.6	273	2	A97700	hypothetical prote
421	68.5	5.7	377	1	J02337	omega-3 fatty acid	494	67.5	5.6	288	2	T23574	conserved hypochet
422	68.5	5.7	383	2	I53870	Edg-1 orphan recep	495	67.5	5.6	320	2	T23574	hypothetical prote
423	68.5	5.7	391	2	H81265	probable transmemb	496	67.5	5.6	323	1	Q08ED3	hypothetical prote
424	68.5	5.7	395	2	B83774	hypothetical prote	497	67.5	5.6	348	2	T12591	hypothetical prote
425	68.5	5.7	395	2	A96189	conserved hypochet	498	67.5	5.6	354	2	T09353	conserved hypochet
426	68.5	5.7	395	2	AH3097	multidrug resistan	499	67.5	5.6	362	2	C88086	hypothetical prote
427	68.5	5.7	419	2	AG1660	Mel-1c receptor su	500	67.5	5.6	387	2	T24581	hypothetical prote
428	68.5	5.7	420	2	I51666	probable glycosylt	501	67.5	5.6	397	2	A83999	mutants block spor
429	68.5	5.7	425	2	F97108	hypothetical prote	502	67.5	5.6	419	2	AH1288	multidrug resistan
430	68.5	5.7	430	2	S15308	preproteinal translo	503	67.5	5.6	439	2	H83699	sodium-dependent C
431	68.5	5.7	441	2	H72247	corticolliberin rec	504	67.5	5.6	450	2	G91219	TDP-FucNAc lipidi
432	68.5	5.7	444	2	A48260	hypothetical prote	505	67.5	5.6	450	2	A86066	TDP-FucNAc lipidi
433	68.5	5.7	445	2	E22845	hypothetical prote	506	67.5	5.6	450	2	F65183	4-alpha-1-fucosylt
434	68.5	5.7	479	2	T44326	hypothetical prote	507	67.5	5.6	452	2	G89870	hypothetical prote
435	68.5	5.7	480	2	E70446	hypothetical prote	508	67.5	5.6	459	2	JH0594	vasoactive intesti
436	68.5	5.7	488	2	T15941	hypothetical prote	509	67.5	5.6	483	2	G84113	hypothetical prote
437	68.5	5.7	492	2	G90574	NADH2 dehydrogenas	510	67.5	5.6	488	1	QXASMA	NADH2 dehydrogenas
438	68.5	5.7	502	2	S77331	probable cytochrom	511	67.5	5.6	492	2	F64464	sodium-dependent n
439	68.5	5.7	512	2	T00605	PAC2 protei	512	67.5	5.6	498	2	T48262	hypothetical prote
440	68.5	5.7	525	2	JN0902	putitrary adenylat	513	67.5	5.6	515	2	E72089	ADP. ATP carrier p
441	68.5	5.7	542	2	S58102	hypothetical prote	514	67.5	5.6	516	2	H82973	choline transpor
442	68.5	5.7	558	2	F64235	Na+ ATPase chain J	515	67.5	5.6	538	2	I51368	gamma-aminobutyric
443	68.5	5.7	634	2	C83530	potassium uptake p	516	67.5	5.6	632	2	A71259	probable dicarboxy
444	68.5	5.7	670	2	G86702	unknown protei	517	67.5	5.6	676	1	W2V218	NPH-II, helicase -
445	68.5	5.7	724	2	H86427	cation-transporin	518	67.5	5.6	676	2	T37345	18r protein - vacc
446	68.5	5.7	768	2	G64707	probable membrane	519	67.5	5.6	676	2	D42511	ATP/GTP-binding pr
447	68.5	5.7	933	1	MMBY7C	probable copper-tr	520	67.5	5.6	676	2	T28500	hypothetical prote
448	68.5	5.7	1004	1	S55353	hypothetical prote	521	67.5	5.6	682	2	D72158	L8r protein - vari
449	68.5	5.7	146	2	H75201	hypothetical prote	522	67.5	5.6	686	2	G82448	sensor histidine k
450	68	5.7	205	2	A64373	hypothetical prote	523	67.5	5.6	716	2	S30687	probable ATP-bindi
451	68	5.7	255	2	F39925	hypothetical prote	524	67.5	5.6	740	1	T02567	probable ATP-bindi
452	68	5.7	266	2	C95316	probable ABC trans	525	67.5	5.6	838	2	A54163	vacuolar ATPase (E
453	68	5.7	270	2	AE3627	mallose transp	526	67.5	5.6	866	2	T20574	hypothetical prote
454	68	5.7	294	2	AG2165	bicarbonate transp	527	67.5	5.6	950	2	T15915	hypothetical prote
455	68	5.7	294	2	T41953	G protein-coupled	528	67.5	5.6	1159	2	T02866	hypothetical prote
456	68	5.7	294	2	AE0004	ribonuclease BN (E	529	67.5	5.6	1244	2	T19615	hypothetical prote
457	68	5.7	313	2	E38888	COI intron 9 prote	530	67.5	5.6	1411	2	S48442	pDRI1 protei
458	68	5.7	335	2	A45177	chemokine (C-C) re	531	67.5	5.6	1753	2	S30855	hypothetical prote
459	68	5.7	360	2	T11067	ubiquitinol-cytochro	532	67.5	5.6	2332	1	GNNYF	genome polyprotein
460	68	5.7	364	2	JC2115	prostaglandin E re	533	67.5	5.6	151	2	A72093	conserved hypochet
461	68	5.7	365	2	JN0693	hypothetical prote	534	67.5	5.6	151	2	H86529	CT101 hypochetical
462	68	5.7	370	2	H90559	hypothetical prote	535	67.5	5.6	180	2	I48129	probable membrane
463	68	5.7	379	2	S58450	ubiquitinol-cytochro	536	67.5	5.6	203	2	D70150	Xel69 (escapes X-1
464	68	5.7	393	2	AG0184	probable multidrug	537	67.5	5.6	225	1	MTIHIIB	hypothetical prote
465	68	5.7	402	2	T41253	hypothetical wtf5	538	67.5	5.6	244	2	D70404	E1 membrane glycop
466	68	5.7	417	2	T11387	NADH2 dehydrogenas	539	67.5	5.6				conserved hypochet
467	68	5.7					540	67.5	5.6				

541	67	5.6	255	2	C90078	hypothetical prote	614	66.5	5.6	412	2	G89773	hypothetical prote
542	67	5.6	275	2	G98194	sugar ABC transpor	615	66.5	5.6	435	2	H95041	polysaccharide tra
543	67	5.6	275	2	AC3092	hypothetical prote	616	66.5	5.6	435	2	D98111	hypothetical prote
544	67	5.6	275	2	S75698	hypothetical prote	617	66.5	5.6	435	2	G95246	malodextrin ABC t
545	67	5.6	276	2	F69307	conserved hypothet	618	66.5	5.6	453	2	B95135	MATE efflux family
546	67	5.6	276	2	S35270	DNA-damage repair	619	66.5	5.6	462	2	H71228	hypothetical prote
547	67	5.6	283	2	F96959	rRNA-processing ri	620	66.5	5.6	488	2	G71969	cytochrome-c oxida
548	67	5.6	285	2	AE3024	hypothetical prote	621	66.5	5.6	490	2	D84998	low-affinity inorg
549	67	5.6	286	2	D64235	hypothetical prote	622	66.5	5.6	490	2	A46391	cAMP receptor subu
550	67	5.6	314	2	D96703	hypothetical prote	623	66.5	5.6	491	2	AC1555	efflux transporter
551	67	5.6	317	2	D98260	inner membrane pro	624	66.5	5.6	493	2	A71875	hypothetical prote
552	67	5.6	336	2	A96997	ferrichrome transp	625	66.5	5.6	494	2	T32644	hypothetical prote
553	67	5.6	345	2	T21776	hypothetical prote	626	66.5	5.6	507	2	T27627	hypothetical prote
554	67	5.6	349	2	D84166	hypothetical prote	627	66.5	5.6	539	2	G83720	nickel transport s
555	67	5.6	350	2	D88987	protein C50H11.2 l	628	66.5	5.6	547	2	E91135	probable alkaline
556	67	5.6	352	2	T32314	hypothetical prote	629	66.5	5.6	550	1	A48026	sterol O-acyltrans
557	67	5.6	379	2	S58451	ubiquinol-cytochro	630	66.5	5.6	582	2	C71424	C-terminal domain
558	67	5.6	379	2	S58449	ubiquinol-cytochro	631	66.5	5.6	583	2	A11510	hypothetical prote
559	67	5.6	396	1	C69291	pheromone shutdow	632	66.5	5.6	598	2	T32430	cytochrome c-type
560	67	5.6	407	2	E70309	hypothetical prote	633	66.5	5.6	603	2	AG2596	cytochrome c-type
561	67	5.6	411	2	B71500	probable amino aci	634	66.5	5.6	603	2	G97478	cytochrome c-type
562	67	5.6	415	2	S74041	pyruvate synthase	635	66.5	5.6	663	2	I56506	Na+/Cl(-)-depend
563	67	5.6	416	2	T46401	hypothetical prote	636	66.5	5.6	727	2	S27043	neurotransmitter t
564	67	5.6	423	2	C95085	sodium-dependent t	637	66.5	5.6	782	2	S19876	genome polyprote
565	67	5.6	436	2	AC1021	proton glutamate s	638	66.5	5.6	862	2	B36786	hypothetical prote
566	67	5.6	441	2	F86279	hypothetical prote	639	66.5	5.6	862	2	T47311	hypothetical prote
567	67	5.6	446	2	G72287	glucose transporte	640	66.5	5.6	889	2	T27479	hypothetical prote
568	67	5.6	456	2	A31986	glycine betaine tr	641	66.5	5.6	992	2	D27479	Na+/Ca2+,K+-exchan
569	67	5.6	507	2	AB1707	probable membrane	642	66.5	5.6	1014	2	C88854	protein F1A10.3 l
570	67	5.6	516	2	AE0665	ATP binding caset	643	66.5	5.6	1083	2	C88854	DNA polymerase III
571	67	5.6	646	2	TC7777	hypothetical prote	644	66.5	5.6	1144	2	H81037	hypothetical prote
572	67	5.6	717	2	T49238	dolichyl-phosphate	645	66.5	5.6	1456	2	T15961	gravin - human
573	67	5.6	753	2	S58331	DNA topoisomerase	646	66.5	5.6	1684	2	UW0057	hypothetical prote
574	67	5.6	769	2	F81415	cell division proc	647	66.5	5.6	1768	2	E85062	genome polyprote
575	67	5.6	784	2	C82679	hypothetical prote	648	66.5	5.6	2151	1	S16449	DNA-directed DNA P
576	67	5.6	787	2	PN0677	hypothetical prote	649	66.5	5.6	2285	1	G02434	inositol 1,4,5-tri
577	67	5.6	798	2	T34248	hypothetical prote	650	66.5	5.6	2833	2	A43360	genome polyprote
578	67	5.6	814	2	T05537	probable serine/tn	651	66.5	5.6	3011	1	GNWYC3	NADH dehydrogenas
579	67	5.6	823	2	T35280	probable integral	652	66.5	5.5	93	2	D28759	diacylglycerol Kin
580	67	5.6	880	2	D69427	conserved hypothet	653	66.5	5.5	130	2	D83820	conserved hypothet
581	67	5.6	891	2	B82495	probable NADH dehy	654	66.5	5.5	209	2	A89801	hypothetical prote
582	67	5.6	900	2	E69631	galactosamine-cont	655	66.5	5.5	276	2	H96816	hypothetical prote
583	67	5.6	1175	2	S39951	chitin synthase (E	656	66.5	5.5	279	2	S42125	hypothetical prote
584	67	5.6	1242	1	DJBECT	DNA-directed DNA p	657	66.5	5.5	285	2	D87447	sulfate ABC transp
585	67	5.6	1333	2	S63403	probable membrane	658	66.5	5.5	302	2	A99074	hypothetical prote
586	67	5.6	1511	2	A53151	pleiotropic drug r	659	66.5	5.5	305	2	B41671	sterol O-acyltrans
587	67	5.6	1575	2	G82905	conserved hypothet	660	66.5	5.5	317	1	B41671	iron transport pro
588	67	5.6	1879	2	T19481	hypothetical prote	661	66.5	5.5	318	2	B84291	hypothetical prote
589	67	5.6	1905	2	T18267	multidrug resistan	662	66.5	5.5	322	2	E71137	hypothetical prote
590	67	5.6	1993	2	T30902	sodium channel SCA	663	66.5	5.5	332	2	C97272	conserved membrane
591	67	5.6	3010	1	GNWVCJ	genome polyprote	664	66.5	5.5	370	1	I52315	G protein-coupled
592	67	5.6	153	1	G69847	conserved hypothet	665	66.5	5.5	379	1	S17405	ubiquinol-cytochro
593	67	5.6	203	2	T28732	hypothetical prote	666	66.5	5.5	379	1	S17405	ubiquinol-cytochro
594	67	5.6	204	2	C70506	hypothetical prote	667	66.5	5.5	379	2	S58460	G protein-coupled
595	67	5.6	218	2	C64586	cag pathogenicity	668	66.5	5.5	381	2	A35300	protein U133 - hum
596	67	5.6	245	2	A81405	sec-independent pr	669	66.5	5.5	390	1	Q08579	hypothetical prote
597	67	5.6	263	2	A12384	hypothetical prote	670	66.5	5.5	397	2	T21154	hypothetical prote
598	67	5.6	268	2	A70417	hypothetical prote	671	66.5	5.5	397	2	T44477	hypothetical prote
599	67	5.6	272	2	A10075	probable permease	672	66.5	5.5	397	2	B70505	probable emulan r
600	67	5.6	279	1	S56642	nitrate transport	673	66.5	5.5	401	2	T44831	probable sugar tra
601	67	5.6	279	2	E70322	hypothetical prote	674	66.5	5.5	404	1	B64927	probable transpor
602	67	5.6	293	2	A84110	sugar ABC transpor	675	66.5	5.5	404	2	A85777	probable transpor
603	67	5.6	294	2	S70876	hypothetical prote	676	66.5	5.5	404	2	E90928	CBS domain prote
604	67	5.6	316	2	F81712	ABC transporter, p	677	66.5	5.5	411	2	H86539	GDEF family prote
605	67	5.6	333	2	S77103	hypothetical prote	678	66.5	5.5	412	2	A82444	hypothetical wtf5
606	67	5.6	347	2	AD2201	hypothetical prote	679	66.5	5.5	418	2	T41027	hypothetical prote
607	67	5.6	356	2	T20737	hypothetical prote	680	66.5	5.5	418	2	B72353	hypothetical prote
608	67	5.6	359	2	E90055	conserved hypothet	681	66.5	5.5	424	2	T07366	probable phosphati
609	67	5.6	367	2	S75836	hypothetical prote	682	66.5	5.5	436	2	T14816	hypothetical prote
610	67	5.6	380	2	G89786	hypothetical prote	683	66.5	5.5	447	2	T18633	alpha-28-adrenergi
611	67	5.6	384	1	I38890	dial specificity p	684	66.5	5.5	450	2	A37223	alpha-2-adrenergi
612	67	5.6	389	2	E96516	PI6N3.13 (imported	685	66.5	5.5	450	2	A38316	ABC transporter pe
613	67	5.6	400	2	G00013	D3 dopamine recepr	686	66.5	5.5	453	2	F86846	ABC transporter pe

687	66	5.5	483	575369	hypothetical prote	760	65.5	5.5	561	2	571189	Dwarf1 protein - A
688	66	5.5	484	T24238	hypothetical prote	761	65.5	5.5	575	2	AH1417	ABC transporter (A
689	66	5.5	486	B82940	hypothetical prote	762	65.5	5.5	578	2	T15736	hypothetical prote
690	66	5.5	508	G47677	hypothetical prote	763	65.5	5.5	583	2	AH1151	glycerophosphoryl
691	66	5.5	525	T28306	ORF MSV15 hypothe	764	65.5	5.5	590	2	C81316	probable sugar epi
692	66	5.5	527	G69635	Prs arbutin-like e	765	65.5	5.5	597	2	B82881	hypothetical prote
693	66	5.5	532	A90037	hypothetical prote	766	65.5	5.5	617	2	B81167	phosphotransferase
694	66	5.5	546	A69890	hypothetical prote	767	65.5	5.5	618	2	AC1204	phosphotransferase
695	66	5.5	548	B87423	cytochrome-c oxida	768	65.5	5.5	642	2	W00331	ATP-dependent heli
696	66	5.5	552	S45866	hypothetical prote	769	65.5	5.5	718	2	A56851	Na+/MgO-inositol c
697	66	5.5	555	S73707	Na(+) translocatin	770	65.5	5.5	720	2	H82198	RTX toxin transpor
698	66	5.5	570	S07744	NADH2 dehydrogenas	771	65.5	5.5	741	2	AF1254	penicillin-binding
699	66	5.5	573	S33212	INDM1 protein - fu	772	65.5	5.5	742	2	SE1568	probable membrane
700	66	5.5	573	AF1418	ABC transporter, A	773	65.5	5.5	860	1	ORHUPD	LDL receptor precu
701	66	5.5	573	AH1793	ABC transporter, A	774	65.5	5.5	958	2	AC0204	probable integral
702	66	5.5	619	T11314	NADH2 dehydrogenas	775	65.5	5.5	1087	1	SA1797	cellulose 1,4-beta
703	66	5.5	632	T24405	hypothetical prote	776	65.5	5.5	1328	2	B42939	TRB protein - yea
704	66	5.5	654	A98350	hypothetical ABC t	777	65.5	5.5	1427	2	S74293	SRB8 protein - yea
705	66	5.5	654	AP2932	hypothetical prote	778	65.5	5.5	1581	2	B71636	hypothetical prote
706	66	5.5	705	T48464	hypothetical prote	779	65.5	5.5	1635	2	T32452	hypothetical prote
707	66	5.5	721	A70754	probable glgX prot	780	65	5.4	126	2	AD0340	probable membrane
708	66	5.5	736	G01522	acidic 82 kDa prot	781	65	5.4	149	2	C69393	transcription regu
709	66	5.5	784	B90442	citron proteinaase	782	65	5.4	176	1	Q1AD25	early E1B 21k prot
710	66	5.5	1039	S76747	hypothetical prote	783	65	5.4	196	2	SA0728	hypothetical prote
711	66	5.5	1054	A61221	probable calcium t	784	65	5.4	225	1	MMIHIV	E1 membrane glycop
712	66	5.5	1359	T34036	hypothetical prote	785	65	5.4	247	2	I48149	serotonin receptor
713	66	5.5	1375	S48375	hypothetical prote	786	65	5.4	257	2	B75099	hypothetical prote
714	66	5.5	2599	F90608	ABC transporter pe	787	65	5.4	259	2	A47112	growth response pr
715	66	5.5	26926	I38344	citin, cardiac mus	788	65	5.4	271	2	B89950	hema concentration
716	65.5	5.5	132	E97760	NADH2 dehydrogenas	789	65	5.4	280	2	S75957	nitrate transport
717	65.5	5.5	132	E70074	hypothetical prote	790	65	5.4	290	2	T02877	probable chlorophy
718	65.5	5.5	146	G69447	hypothetical prote	791	65	5.4	291	2	C97453	cytochrome c oxida
719	65.5	5.5	171	A13476	signal peptidase I	792	65	5.4	291	2	AE2671	cytochrome c oxida
720	65.5	5.5	197	T17106	hypothetical prote	793	65	5.4	307	2	B36125	branched-chain ami
721	65.5	5.5	210	S67771	endoplasmic reticu	794	65	5.4	313	2	AC4084	lysophospholipase
722	65.5	5.5	252	T43100	hypothetical prote	795	65	5.4	319	2	D87087	hypothetical prote
723	65.5	5.5	290	F69456	signal sequence pe	796	65	5.4	322	2	S38091	hypothetical prote
724	65.5	5.5	297	F86839	phosphate ABC tran	797	65	5.4	330	2	H75068	dipeptide abc tran
725	65.5	5.5	297	E83792	hypothetical prote	798	65	5.4	335	2	H75029	hypothetical prote
726	65.5	5.5	301	T21308	hypothetical prote	799	65	5.4	338	2	S50339	NADH2 dehydrogenas
727	65.5	5.5	317	S23459	polyanilide reduct	800	65	5.4	344	2	AD1200	conserved hypotnet
728	65.5	5.5	327	T32607	probable binding p	801	65	5.4	345	2	T12361	NADH2 dehydrogenas
729	65.5	5.5	348	S36003	NADH2 dehydrogenas	802	65	5.4	355	2	G70200	hypothetical prote
730	65.5	5.5	351	F82880	hypothetical ferrit	803	65	5.4	359	2	T15249	hypothetical prote
731	65.5	5.5	365	F69629	spore germination	804	65	5.4	362	2	H69785	mannan endo-1,4-be
732	65.5	5.5	367	JC2056	prostaglandin E2 r	805	65	5.4	375	2	T38879	corticotropin rele
733	65.5	5.5	379	S58456	ubiquinol-cytochro	806	65	5.4	379	1	S17414	ubiquinol-cytochro
734	65.5	5.5	379	T32778	hypothetical prote	807	65	5.4	379	2	S58461	ubiquinol-cytochro
735	65.5	5.5	391	T32601	hypothetical prote	808	65	5.4	379	2	S58455	ubiquinol-cytochro
736	65.5	5.5	394	AH0362	nucleoside permas	809	65	5.4	380	1	D34285	ubiquinol-cytochro
737	65.5	5.5	410	T11064	NADH2 dehydrogenas	810	65	5.4	382	2	T11138	ubiquinol-cytochro
738	65.5	5.5	423	B80569	conserved hypotnet	811	65	5.4	390	2	C84984	hypothetical prote
739	65.5	5.5	425	A97688	hypothetical 45.5K	812	65	5.4	415	2	T21532	hypothetical prote
740	65.5	5.5	425	AF2913	conserved hypotnet	813	65	5.4	438	2	B81410	probable integral
741	65.5	5.5	429	T32832	microfibril-associ	814	65	5.4	442	2	AD3122	probable MFS trans
742	65.5	5.5	442	A42670	probable transcrip	815	65	5.4	445	2	AD2358	glucosyltransferas
743	65.5	5.5	445	T38916	probable dicarboxy	816	65	5.4	457	2	T28334	Ser/Thr protein ki
744	65.5	5.5	449	A83629	hypothetical prote	817	65	5.4	462	2	B88613	protein T37E9.5 (I
745	65.5	5.5	457	B75327	hypothetical prote	818	65	5.4	477	2	S54508	probable membrane
746	65.5	5.5	477	B75170	hypothetical prote	819	65	5.4	477	2	A69036	TRK system potassi
747	65.5	5.5	480	A60043	endoplasmic reticu	820	65	5.4	481	2	B81050	cytochrome-c oxida
748	65.5	5.5	487	A97928	type I site-specific	821	65	5.4	490	2	T14545	probable sugar tra
749	65.5	5.5	488	H64537	cytochrome-c oxida	822	65	5.4	492	2	S59107	NADH2 dehydrogenas
750	65.5	5.5	488	G81295	cytochrome-c oxida	823	65	5.4	510	2	S55204	hypothetical prote
751	65.5	5.5	491	A61197	efflux transporter	824	65	5.4	511	2	H75097	polysaccharide bio
752	65.5	5.5	495	A97022	probably membrane	825	65	5.4	513	2	T37180	probable membrane
753	65.5	5.5	495	G84706	hypothetical prote	826	65	5.4	526	2	D91047	hydrogenase 4 memb
754	65.5	5.5	502	AD3395	NADH2 dehydrogenas	827	65	5.4	530	2	B89771	hypothetical prote
755	65.5	5.5	502	T25669	hypothetical prote	828	65	5.4	535	2	A64697	conserved hypotnet
756	65.5	5.5	518	A53207	probable folate tr	829	65	5.4	539	2	S55190	hypothetical prote
757	65.5	5.5	528	T34417	delayed rectifier	830	65	5.4	547	2	T31543	hypothetical prote
758	65.5	5.5	544	B84825	probable ABC trans	831	65	5.4	547	2	S53920	SNK1 protein - yea
759	65.5	5.5	545	B90460	hypothetical prote	832	65	5.4	576	2	T25375	hypothetical prote

833	65	5.4	579	2	S61131	probable membrane
834	65	5.4	608	2	S65298	dicarboxylic amino
835	65	5.4	611	2	T21747	hypothetical prote
836	65	5.4	624	2	G82508	hypothetical prote
837	65	5.4	627	2	T11125	NADH2 dehydrogenas
838	65	5.4	633	2	F84483	Mutator-like trans
839	65	5.4	638	2	D69957	conserved hypotet
840	65	5.4	643	2	F97787	sodium/pantothenat
841	65	5.4	676	2	A45515	diak-type molecula
842	65	5.4	684	2	F86394	protein T24P13.20
843	65	5.4	697	2	H84791	hypothetical prote
844	65	5.4	702	2	T11505	NADH2 dehydrogenas
845	65	5.4	705	2	T04400	NADH2 dehydrogenas
846	65	5.4	773	2	H96818	hypothetical prote
847	65	5.4	773	2	G83816	late competence op
848	65	5.4	808	2	T00459	hypothetical prote
849	65	5.4	861	2	S77086	hypothetical prote
850	65	5.4	927	2	T38518	ribonuclease II RN
851	65	5.4	931	2	F84637	probable plasma, me
852	65	5.4	938	2	T01809	hypothetical prote
853	65	5.4	1089	2	C70522	probable mmp18 pro
854	65	5.4	1163	2	D64315	type I restriction
855	65	5.4	1178	2	S76370	sensory transducti
856	65	5.4	1232	2	T38496	anion exchanger 3
857	65	5.4	1421	2	T34225	hypothetical prote
858	65	5.4	5069	2	T17464	riifamycin polypept
859	64.5	5.4	180	2	T41339	hypothetical prote
860	64.5	5.4	211	2	S35280	eac protein - phag
861	64.5	5.4	217	2	AE0395	probable amino aci
862	64.5	5.4	227	2	C69432	hypothetical prote
863	64.5	5.4	234	2	B96957	NAD superfamily hy
864	64.5	5.4	268	2	AP2470	potassium channel
865	64.5	5.4	271	2	E81384	prolipo protein dia
866	64.5	5.4	275	2	T43119	hypothetical prote
867	64.5	5.4	293	2	D71517	probable metal tra
868	64.5	5.4	295	2	T32022	hypothetical prote
869	64.5	5.4	297	2	T27584	hypothetical prote
870	64.5	5.4	320	2	T23904	hypothetical prote
871	64.5	5.4	326	2	A86411	protein F3M18.6 [1
872	64.5	5.4	353	2	F64175	hypothetical prote
873	64.5	5.4	358	2	T22823	hypothetical prote
874	64.5	5.4	361	2	A86841	hypothetical prote
875	64.5	5.4	361	2	A40734	Pa (Passover) pro
876	64.5	5.4	379	1	S43264	ubiquinol-cytochro
877	64.5	5.4	379	1	T11505	ubiquinol-cytochro
878	64.5	5.4	379	2	S58454	ubiquinol-cytochro
879	64.5	5.4	379	2	A53077	ubiquinol-cytochro
880	64.5	5.4	381	1	CBMS	ubiquinol-cytochro
881	64.5	5.4	381	2	S33449	plutitary adenylat
882	64.5	5.4	385	2	H69154	hypothetical prote
883	64.5	5.4	398	2	H95057	phosphoglycerate k
884	64.5	5.4	398	2	A97927	phosphoglycerate k
885	64.5	5.4	400	2	G01977	d3 dopamine recept
886	64.5	5.4	411	2	S46800	LAG1 protein - yea
887	64.5	5.4	416	2	AF1127	rod shape-determin
888	64.5	5.4	426	2	T45800	UDP-N-acetylglucos
889	64.5	5.4	433	2	T11162	NADH2 dehydrogenas
890	64.5	5.4	435	2	AC0105	probable maltodext
891	64.5	5.4	439	2	C22845	NADH2 dehydrogenas
892	64.5	5.4	439	2	A84153	hypothetical prote
893	64.5	5.4	443	2	B26636	hypothetical prote
894	64.5	5.4	444	2	T11474	NADH2 dehydrogenas
895	64.5	5.4	444	2	A43676	P4 heparitis-asso
896	64.5	5.4	444	2	S48218	microtubular aggre
897	64.5	5.4	446	1	DYRTD3	dopamine receptor
898	64.5	5.4	448	2	S57909	hypothetical prote
899	64.5	5.4	448	2	S57909	probable histidine
900	64.5	5.4	450	2	T23528	hypothetical prote
901	64.5	5.4	451	2	D70045	two-component sens
902	64.5	5.4	467	2	JN0616	plutitary adenylat
903	64.5	5.4	478	2	C29051	crnspasease C - Ba
904	64.5	5.4	495	1	FWSYCG2	glyciclin chain Ala
905	64.5	5.4	495	2	S39061	plutitary adenylat
906	64.5	5.4	495	2	S36114	plutitary adenylat
907	64.5	5.4	495	2	S10851	glyciclin GI precur
908	64.5	5.4	512	2	H64864	probable membrane
909	64.5	5.4	521	2	A49549	amino acid permeas
910	64.5	5.4	523	2	S39060	plutitary adenylat
911	64.5	5.4	547	2	H65107	hypothetical 61.6
912	64.5	5.4	554	2	A56730	carl protein - Pod
913	64.5	5.4	555	2	B97812	virulence factor m
914	64.5	5.4	575	2	AB1793	ABC transporter (A
915	64.5	5.4	576	2	T05904	cytochrome P450 97
916	64.5	5.4	614	2	B89869	hypothetical prote
917	64.5	5.4	622	2	AC1236	acyltansferase (t
918	64.5	5.4	638	1	OC8Y2M	mRNA maturase b14
919	64.5	5.4	715	2	T26307	hypothetical prote
920	64.5	5.4	720	2	T47648	ABC transporter-11
921	64.5	5.4	721	2	AD1617	penicillin-binding
922	64.5	5.4	721	2	AE1491	hypothetical prote
923	64.5	5.4	735	2	AD0341	probable membrane
924	64.5	5.4	763	2	AD1070	phosphatidylglycer
925	64.5	5.4	801	2	A89862	Na+/H+ antiporter
926	64.5	5.4	803	2	H64568	histidine kinase -
927	64.5	5.4	889	2	T30715	probable major cor
928	64.5	5.4	979	2	A70848	probable membrane
929	64.5	5.4	1007	2	JC8066	138k protein - Tet
930	64.5	5.4	1114	2	JH0284	125k surface antiq
931	64.5	5.4	1146	2	B70723	probable mmp12 pr
932	64.5	5.4	1154	2	T48829	related to GREP C
933	64.5	5.4	1465	2	S45628	DNA-directed DNA p
934	64.5	5.4	1529	2	S69688	hypothetical prote
935	64.5	5.4	1630	2	S64403	ESPI protein - Yea
936	64.5	5.4	1661	2	S64800	probable membrane
937	64.5	5.4	3033	1	GNWY78	genome polyprotein
938	64.5	5.4	202	2	A70041	conserved hypotet
939	64.5	5.4	209	2	G82359	conserved hypotet
940	64.5	5.4	253	2	JC5347	cdd3 protein - Clo
941	64.5	5.4	259	2	T12451	hypothetical prote
942	64.5	5.4	269	2	H69768	conserved hypotet
943	64.5	5.4	270	2	F89632	protein F13B6.3 [1
944	64.5	5.4	274	2	T50567	probable ABC-type
945	64.5	5.4	276	2	C70040	plant-metabolite d
946	64.5	5.4	281	2	S48358	probable membrane
947	64.5	5.4	281	2	EA9532	probable sugar upt
948	64.5	5.4	283	2	D83009	probable permease
949	64.5	5.4	285	2	B83883	sugar transport sy
950	64.5	5.4	288	2	S36955	cytochrome-c oxida
951	64.5	5.4	330	2	T29675	hypothetical prote
952	64.5	5.4	342	2	A48258	dopamine receptor
953	64.5	5.4	347	2	T11248	NADH2 dehydrogenas
954	64.5	5.4	351	2	S56716	protein kinase SPK
955	64.5	5.4	351	2	G01430	Pl6 protein - huma
956	64.5	5.4	367	2	T20271	hypothetical prote
957	64.5	5.4	369	2	H90587	hypothetical prote
958	64.5	5.4	370	1	S26031	ubiquinol-cytochro
959	64.5	5.4	376	2	G82656	twilching motility
960	64.5	5.4	378	2	D64181	probable cytochrom
961	64.5	5.4	379	1	CBBO	ubiquinol-cytochro
962	64.5	5.4	379	1	S17419	ubiquinol-cytochro
963	64.5	5.4	379	1	S26163	ubiquinol-cytochro
964	64.5	5.4	379	1	S43263	ubiquinol-cytochro
965	64.5	5.4	379	2	T11414	ubiquinol-cytochro
966	64.5	5.4	379	2	S58452	ubiquinol-cytochro
967	64.5	5.4	379	2	S58459	ubiquinol-cytochro
968	64.5	5.4	383	2	S55354	G protein-coupled
969	64.5	5.4	383	2	G64667	Na+/H+ antiporter
970	64.5	5.4	383	2	H71848	probable na+/h+ an
971	64.5	5.4	387	2	S74532	hypothetical prote
972	64.5	5.4	402	2	AD1417	drug-efflux transp
973	64.5	5.4	404	2	A97559	hypothetical prote
974	64.5	5.4	404	2	AE2779	acyltansferase [i
975	64.5	5.4	409	2	S26021	NADH2 dehydrogenas
976	64.5	5.4	411	2	A55610	corticotropin-rele
977	64.5	5.4	413	2	H81659	branched-chain ami
978	64.5	5.4	422	2	E84338	isocitrate dehydro

979	64	5.4	430	1	S32570	malC protein - Str	1052	63.5	5.3	327	2	S56162	MDCR15 protein - h
980	64	5.4	450	2	D40392	alpha-2-adrenergic	1053	63.5	5.3	328	2	D98215	oligopeptide ABC t
981	64	5.4	451	2	A36098	spore cortex penic	1054	63.5	5.3	328	2	T39824	septicin homolog - f
982	64	5.4	455	2	T31258	atrometic OXygenase	1055	63.5	5.3	334	2	B72393	oligopeptide ABC t
983	64	5.4	457	2	AF2975	aminoctransferrase,	1056	63.5	5.3	334	2	T41037	hypothetical prote
984	64	5.4	457	2	E98307	probable aminotran	1057	63.5	5.3	334	2	T27081	hypothetical prote
985	64	5.4	463	2	AC0281	probable amino aci	1058	63.5	5.3	342	2	A38908	spaa40 protein - Sh
986	64	5.4	469	2	H90322	polyaccharide bico	1059	63.5	5.3	344	2	T34981	probable integral
987	64	5.4	492	2	E58931	NMDH2 dehydrogenas	1060	63.5	5.3	355	2	T15203	hypothetical prote
988	64	5.4	492	2	JC7627	cytochrome P450 3A	1061	63.5	5.3	359	2	D90172	hypothetical prote
989	64	5.4	511	2	T40334	hypothetical prote	1062	63.5	5.3	361	2	AE3071	hypothetical prote
990	64	5.4	527	2	A75122	sodium- and chlori	1063	63.5	5.3	365	2	AB3494	oligopeptide trans
991	64	5.4	536	2	T36109	hypothetical prote	1064	63.5	5.3	372	2	S2667	G protein-coupled
992	64	5.4	538	2	C90406	conserved hypotet	1065	63.5	5.3	377	2	B72275	probable aspartate
993	64	5.4	544	2	T13877	NMDH2 dehydrogenas	1066	63.5	5.3	380	1	CBRT	ubiquinol-cytocho
994	64	5.4	552	2	T52481	cytochrome-c oxida	1067	63.5	5.3	381	2	T11312	ubiquinol-cytocho
995	64	5.4	552	2	G75282	probable glutathio	1068	63.5	5.3	387	2	H88012	protein K1054.2 [i
996	64	5.4	566	1	A34400	ezrin [validated]	1069	63.5	5.3	389	2	G75133	hypothetical prote
997	64	5.4	586	1	T05130	hypothetical prote	1070	63.5	5.3	392	2	H71520	probable hth trans
998	64	5.4	598	2	C75120	hypothetical prote	1071	63.5	5.3	395	2	B81358	transmembrane tran
999	64	5.4	602	2	B69805	conserved hypotet	1072	63.5	5.3	398	2	C71682	ubiquinol-cytocho
1000	64	5.4	606	2	C02640	polycystic kidney	1073	63.5	5.3	398	2	D81397	probable periplasm
1001	64	5.4	608	2	F70512	probable ATPase -	1074	63.5	5.3	399	2	B95080	cell division prot
1002	64	5.4	610	2	S37049	H+-exporting ATPas	1075	63.5	5.3	400	2	AG3016	phosphoglycerate k
1003	64	5.4	614	2	A69845	Na+/H+ antiporter	1076	63.5	5.3	401	1	T46306	hypothetical prote
1004	64	5.4	630	2	T47177	hypothetical prote	1077	63.5	5.3	404	2	LABECA	latent membrane pr
1005	64	5.4	644	2	C86677	DNA ligase (NAD) (	1078	63.5	5.3	406	2	T19887	hypothetical prote
1006	64	5.4	657	2	T52460	hypothetical prote	1079	63.5	5.3	423	2	T04915	CBP-diacylglycerol
1007	64	5.4	661	2	T51779	non-phototropic hy	1080	63.5	5.3	423	2	C85255	CBP-diacylglycerol
1008	64	5.4	674	2	T50347	hypothetical prote	1081	63.5	5.3	426	2	A96268	phosphoglycerate k
1009	64	5.4	696	2	AB1566	hypothetical prote	1082	63.5	5.3	436	2	T33299	hypothetical prote
1010	64	5.4	748	2	T10651	hypothetical prote	1083	63.5	5.3	438	2	A82262	conserved hypotet
1011	64	5.4	802	2	A87754	protein C43R1.11	1084	63.5	5.3	444	2	B85789	hypothetical prote
1012	64	5.4	838	2	H82939	conserved hypotet	1085	63.5	5.3	445	2	T16025	hypothetical prote
1013	64	5.4	860	2	T37768	probable vacuolar	1086	63.5	5.3	447	2	F90940	hypothetical prote
1014	64	5.4	874	2	B86322	FA14.8 protein -	1087	63.5	5.3	447	2	S52437	CBP-diacylglycerol
1015	64	5.4	896	2	AF1409	the two components	1088	63.5	5.3	450	2	E96738	hypothetical prote
1016	64	5.4	991	2	S57385	probable membrane	1089	63.5	5.3	452	2	T21118	hypothetical prote
1017	64	5.4	1024	1	RN208F	DNA-directed RNA p	1090	63.5	5.3	461	2	C97187	sugar transferase
1018	64	5.4	1078	2	T19745	hypothetical prote	1091	63.5	5.3	468	2	T48686	hypothetical prote
1019	64	5.4	1081	2	B81303	probable membrane	1092	63.5	5.3	485	2	H90552	mg2+ transport pro
1020	64	5.4	1227	2	A33638	erythrocyte anion	1093	63.5	5.3	487	2	B95059	hypothetical prote
1021	64	5.4	1385	2	T13415	hypothetical prote	1094	63.5	5.3	491	2	A64939	hypothetical prote
1022	64	5.4	1462	1	DJHMAC	DNA-directed DNA p	1095	63.5	5.3	492	2	B90373	sugar transport re
1023	64	5.4	1695	2	J80084	voltage-gated sodi	1096	63.5	5.3	494	2	S76516	integral membrane
1024	64	5.4	2496	2	A71616	secreted protein p	1097	63.5	5.3	498	2	T48385	transporter like p
1025	63.5	5.3	111	2	S43115	acidic ribosomal p	1098	63.5	5.3	498	2	T61890	hypothetical prote
1026	63.5	5.3	123	2	G71692	NMDH2 dehydrogenas	1099	63.5	5.3	500	2	AF2325	NMDH dehydrogenase
1027	63.5	5.3	147	2	AH0495	probable membrane	1100	63.5	5.3	511	2	G90321	hypothetical prote
1028	63.5	5.3	149	2	H70581	hypothetical prote	1101	63.5	5.3	512	1	A70201	virulence factor m
1029	63.5	5.3	195	2	E71000	hypothetical prote	1102	63.5	5.3	525	2	A49601	nucleoside prote
1030	63.5	5.3	214	2	C90191	conserved hypotet	1103	63.5	5.3	537	2	G82873	conserved hypotet
1031	63.5	5.3	218	2	B71925	cag island protein	1104	63.5	5.3	540	1	T49454	sterol O-acetyltrans
1032	63.5	5.3	231	2	T29205	hypothetical prote	1105	63.5	5.3	544	2	C96943	uncharacterized me
1033	63.5	5.3	238	2	F85679	probable antipept	1106	63.5	5.3	551	2	E64537	L-lactate permease
1034	63.5	5.3	238	2	S75336	hypothetical prote	1107	63.5	5.3	551	2	D71969	L-lactate permease
1035	63.5	5.3	241	2	F86691	ABC transporter pe	1108	63.5	5.3	555	2	G96744	probable peptidase
1036	63.5	5.3	242	1	S74794	hypothetical prote	1109	63.5	5.3	567	2	C75340	probable L-lactate
1037	63.5	5.3	246	2	AD3574	branched-chain ami	1110	63.5	5.3	568	2	T17588	hyaluronoglucosami
1038	63.5	5.3	259	2	AF0106	probable membrane	1111	63.5	5.3	593	2	T16528	sodium/dicarboxyla
1039	63.5	5.3	275	2	E95161	hypothetical prote	1112	63.5	5.3	594	2	E88956	protein ZK697.5 [i
1040	63.5	5.3	275	2	D98027	hypothetical prote	1113	63.5	5.3	605	2	A36361	glucose transport
1041	63.5	5.3	275	2	G84330	hypothetical prote	1114	63.5	5.3	605	2	H71562	probable flagellar
1042	63.5	5.3	276	2	E96951	conserved membrane	1115	63.5	5.3	605	2	T43974	hypothetical prote
1043	63.5	5.3	280	2	T16240	hypothetical prote	1116	63.5	5.3	610	2	T44161	hypothetical prote
1044	63.5	5.3	282	2	E83086	conserved hypotet	1117	63.5	5.3	668	2	B54759	ba-type ubiquinol
1045	63.5	5.3	282	2	AB0346	probable ABC trans	1118	63.5	5.3	671	2	B37627	protein kinase C (
1046	63.5	5.3	291	2	AB2939	hypothetical prote	1119	63.5	5.3	681	2	AF0697	probable type iii
1047	63.5	5.3	291	2	E98343	hypothetical prote	1120	63.5	5.3	683	2	A85044	hypothetical prote
1048	63.5	5.3	291	2	F75571	hypothetical prote	1121	63.5	5.3	708	2	J01148	killer toxin KHS p
1049	63.5	5.3	313	2	D26696	NMDH2 dehydrogenas	1122	63.5	5.3	741	2	T20334	hypothetical prote
1050	63.5	5.3	315	2	E69365	hypothetical prote	1123	63.5	5.3	780	2	T48189	probable transport
1051	63.5	5.3	316	2	H86665	ferrichrome ABC tr	1124	63.5	5.3	787	2	A70132	cell division prot

1125	63.5	5.3	819	2	T19351	1198	63	5.3	480	2	B70367	hypothetical prote
1126	63.5	5.3	841	2	T38703	1199	63	5.3	481	2	S60260	stomatin-like prot
1127	63.5	5.3	843	2	T32487	1200	63	5.3	480	2	C71541	probable na-depend
1128	63.5	5.3	843	2	T41237	1201	63	5.3	491	2	AC1499	transmembrane prot
1129	63.5	5.3	844	2	AD2339	1202	63	5.3	493	2	T02376	hypothetical prote
1130	63.5	5.3	951	2	T08997	1203	63	5.3	494	2	T14246	NADH2 dehydrogenas
1131	63.5	5.3	966	2	H97717	1204	63	5.3	508	1	E90594	amino acid permeas
1132	63.5	5.3	1004	2	G87333	1205	63	5.3	509	1	A48528	membrane glycoprot
1133	63.5	5.3	1004	2	S38100	1206	63	5.3	527	2	T40744	probable nuclear d
1134	63.5	5.3	1098	2	S42391	1207	63	5.3	531	2	AH1491	hypothetical prote
1135	63.5	5.3	1229	2	C71607	1208	63	5.3	533	2	T06153	hypothetical prote
1136	63.5	5.3	1351	2	T17269	1209	63	5.3	534	2	AF9316	hypothetical prote
1137	63.5	5.3	1388	2	T17269	1210	63	5.3	535	2	AF1835	hypothetical prote
1138	63.5	5.3	1407	1	T00558	1210	63	5.3	552	2	B70081	hypothetical prote
1139	63.5	5.3	1408	1	T47671	1211	63	5.3	552	2	B70081	protein Simlar to
1140	63.5	5.3	1545	2	T42751	1212	63	5.3	559	2	B86359	flageellar basal-bo
1141	63.5	5.3	1545	2	T46645	1213	63	5.3	569	2	C70136	hypothetical prote
1142	63.5	5.3	1769	2	S53378	1214	63	5.3	574	2	T47566	hypothetical prote
1143	63.5	5.3	2357	2	A59249	1215	63	5.3	579	2	AB2177	probable PPR2 fami
1144	63.5	5.3	4725	1	A44357	1216	63	5.3	583	2	G84829	two-component sens
1145	63	5.3	96	1	MMV2P3	1217	63	5.3	584	2	G89789	probable membrane
1146	63	5.3	103	2	T20878	1218	63	5.3	598	2	S66954	two-component sens
1147	63	5.3	175	2	D70945	1219	63	5.3	600	2	B83875	ABC transporter At
1148	63	5.3	230	2	B81705	1220	63	5.3	608	2	AD2000	hypothetical prote
1149	63	5.3	230	2	T17506	1221	63	5.3	677	2	T26574	probable membrane-
1150	63	5.3	236	2	F83520	1222	63	5.3	677	2	P95910	replication licens
1151	63	5.3	249	2	T01891	1223	63	5.3	682	1	H64485	NADH2 dehydrogenas
1152	63	5.3	257	2	S01165	1224	63	5.3	701	2	T13568	NADH2 dehydrogenas
1153	63	5.3	258	2	H65188	1225	63	5.3	702	2	T12677	NADH2 dehydrogenas
1154	63	5.3	258	2	S61861	1226	63	5.3	712	2	T13665	proton pump, proba
1155	63	5.3	280	2	S48301	1227	63	5.3	729	2	D87418	probable sugar tra
1156	63	5.3	288	2	S48301	1228	63	5.3	729	2	T39547	S-protein secretio
1157	63	5.3	290	2	S48301	1229	63	5.3	738	2	S58612	NADH2 dehydrogenas
1158	63	5.3	301	2	T50001	1230	63	5.3	769	2	G95270	hypothetical prote
1159	63	5.3	305	2	H83620	1231	63	5.3	813	2	T02672	hypothetical prote
1160	63	5.3	313	2	A86743	1232	63	5.3	849	2	C87740	protein H26D21.2 [
1161	63	5.3	322	2	B90013	1233	63	5.3	869	2	S49844	probable membrane
1162	63	5.3	329	2	B87790	1234	63	5.3	943	2	B15082	neurotrophic recep
1163	63	5.3	332	2	B84943	1235	63	5.3	960	2	T17287	hypothetical prote
1164	63	5.3	339	2	D89880	1236	63	5.3	1030	2	A42497	anion exchanger 3,
1165	63	5.3	345	2	T12364	1237	63	5.3	1034	2	B86880	SWI/SNF family hel
1166	63	5.3	358	2	B83808	1238	63	5.3	1082	2	H70360	cation efflux syst
1167	63	5.3	359	2	S56720	1239	63	5.3	1212	2	B82809	exodeoxyribonuclea
1168	63	5.3	361	2	A45211	1240	63	5.3	1227	2	B34911	band 3-related pro
1169	63	5.3	362	2	C69804	1241	63	5.3	1332	2	T18438	hypothetical prote
1170	63	5.3	364	2	T29552	1242	63	5.3	1532	2	UH0422	voltage-dependent
1171	63	5.3	364	2	S65009	1243	63	5.3	1646	2	T39035	putative sodium ch
1172	63	5.3	365	2	A42414	1244	63	5.3	1854	2	T42742	voltage-dependent
1173	63	5.3	378	1	S17412	1245	63	5.3	2203	2	B71621	probable membrane
1174	63	5.3	379	1	S17411	1246	63	5.3	2295	2	RR1HW2	genome polypotein
1175	63	5.3	379	1	S41847	1247	63	5.3	4488	1	RR1HW2	hypothetical prote
1176	63	5.3	379	1	S41833	1248	62.5	5.2	107	2	B69282	potassium channel
1177	63	5.3	379	1	S41833	1249	62.5	5.2	140	2	B86739	hypothetical prote
1178	63	5.3	379	2	S58085	1250	62.5	5.2	149	2	B83851	DNA-damage-inducib
1179	63	5.3	379	2	S58085	1251	62.5	5.2	168	2	JC1169	hypothetical prote
1180	63	5.3	382	2	S58464	1252	62.5	5.2	178	2	D71702	hypothetical prote
1181	63	5.3	382	2	S47882	1253	62.5	5.2	181	2	G82911	hypothetical prote
1182	63	5.3	386	2	S60646	1254	62.5	5.2	200	2	A71895	hypothetical prote
1183	63	5.3	389	2	H95003	1255	62.5	5.2	232	2	T22698	hypothetical prote
1184	63	5.3	389	2	C97876	1256	62.5	5.2	236	2	F83705	hypothetical prote
1185	63	5.3	391	2	D64541	1257	62.5	5.2	240	2	H70091	hypothetical prote
1186	63	5.3	396	2	E97947	1258	62.5	5.2	244	2	T20810	hypothetical prote
1187	63	5.3	396	2	B70415	1259	62.5	5.2	245	2	S10658	hypothetical prote
1188	63	5.3	405	2	T20902	1260	62.5	5.2	258	2	E91201	type III secretion
1189	63	5.3	411	2	G90154	1261	62.5	5.2	258	2	A86048	ect (imported) -
1190	63	5.3	415	2	S39535	1262	62.5	5.2	274	2	AC2946	hypothetical prote
1191	63	5.3	420	2	A57742	1263	62.5	5.2	274	2	G98136	glycerol-3-phospha
1192	63	5.3	431	2	T23809	1264	62.5	5.2	276	2	G72292	sorbitol/mannitol
1193	63	5.3	448	2	T30982	1265	62.5	5.2	276	2	H83568	probable permease
1194	63	5.3	450	2	A34169	1266	62.5	5.2	280	2	T24579	hypothetical prote
1195	63	5.3	460	2	A62188	1267	62.5	5.2	283	2	T11063	NADH2 dehydrogenas
1196	63	5.3	475	2	S52893	1268	62.5	5.2	289	2	D82504	phosphate ABC tran
1197	63	5.3	478	2	C59095	1270	62.5	5.2	293	2	AH0075	probable permease



1271	62.5	5.2	296	2	H83480	1344	62.5	5.2	704	2	S46000	probable membrane
1272	62.5	5.2	298	2	T37251	1345	62.5	5.2	718	2	T05840	subtilisin-like pr
1273	62.5	5.2	299	2	T26365	1346	62.5	5.2	763	2	T27937	hypothetical prote
1274	62.5	5.2	326	2	C90272	1347	62.5	5.2	807	2	T28279	ORF MSV19 probabl
1275	62.5	5.2	333	2	AB1925	1348	62.5	5.2	815	2	G97266	mannose-1-phosphat
1276	62.5	5.2	333	2	B89010	1349	62.5	5.2	837	2	D71027	hypothetical prote
1277	62.5	5.2	335	2	T41426	1350	62.5	5.2	848	2	A33810	band 3 anion trans
1278	62.5	5.2	349	2	H95060	1351	62.5	5.2	865	2	AB1658	probable membrane
1279	62.5	5.2	349	2	D97929	1352	62.5	5.2	881	2	G96574	hypothetical prote
1280	62.5	5.2	352	2	E81450	1353	62.5	5.2	971	2	H71719	hypothetical prote
1281	62.5	5.2	358	2	E83829	1354	62.5	5.2	1082	2	T41988	hypothetical prote
1282	62.5	5.2	365	2	F82210	1355	62.5	5.2	1144	2	AB1983	probable DNA-direc
1283	62.5	5.2	369	2	C88030	1356	62.5	5.2	1195	2	C87691	hypothetical prote
1284	62.5	5.2	370	2	C69309	1357	62.5	5.2	1291	2	T17242	hypothetical prote
1285	62.5	5.2	379	1	S17407	1358	62.5	5.2	1391	2	T20642	hypothetical prote
1286	62.5	5.2	379	2	S58462	1359	62.5	5.2	1397	2	E87998	protein F09C3.1 [1
1287	62.5	5.2	379	2	S58057	1360	62.5	5.2	1576	2	T21172	hypothetical prote
1288	62.5	5.2	382	2	A72373	1361	62.5	5.2	1676	2	E71410	probable centromer
1289	62.5	5.2	383	1	A44227	1362	62.5	5.2	1687	2	T43144	vitellogenin II pr
1290	62.5	5.2	383	2	F84771	1363	62.5	5.2	1951	2	B43963	RNA viral polymera
1291	62.5	5.2	383	2	T31738	1364	62.5	5.2	2150	2	S13553	hypothetical prote
1292	62.5	5.2	388	2	C64722	1365	62.5	5.2	1132	2	T11073	NADH2 dehydrogenas
1293	62.5	5.2	391	2	A86532	1366	62.5	5.2	132	2	D82854	hypothetical prote
1294	62.5	5.2	399	2	H84087	1367	62.5	5.2	174	2	E84028	cell-shape determi
1295	62.5	5.2	404	2	H83249	1368	62.5	5.2	175	1	IMECB	colicin B immunity
1296	62.5	5.2	405	1	QOBB35	1369	62.5	5.2	198	2	E97217	uncharacterized co
1297	62.5	5.2	406	2	H89006	1370	62.5	5.2	201	2	G90134	hypothetical prote
1298	62.5	5.2	409	2	C89942	1371	62.5	5.2	206	2	F89840	conserved hypochet
1299	62.5	5.2	413	2	AC1369	1372	62.5	5.2	209	2	A89656	protein F37C4.1 [1
1300	62.5	5.2	417	2	T51467	1373	62.5	5.2	209	2	T32573	hypothetical prote
1301	62.5	5.2	420	2	D95018	1374	62.5	5.2	225	2	B65127	type 4 prephilin-11
1302	62.5	5.2	420	2	E97891	1375	62.5	5.2	242	1	F75433	probable phosphoes
1303	62.5	5.2	422	2	C70518	1376	62.5	5.2	247	2	AC1332	potassium channel
1304	62.5	5.2	425	2	E97172	1377	62.5	5.2	273	2	E70010	dihydrolipoamide S
1305	62.5	5.2	426	2	A72080	1378	62.5	5.2	285	2	H95943	probable sugar upc
1306	62.5	5.2	426	2	E86542	1379	62.5	5.2	287	2	A69838	transcription regu
1307	62.5	5.2	431	2	H84069	1380	62.5	5.2	288	2	S36953	cytochrome-c oxida
1308	62.5	5.2	440	2	T20092	1381	62.5	5.2	288	2	C83156	probable permease
1309	62.5	5.2	442	1	J01042	1382	62.5	5.2	298	2	T29189	hypothetical prote
1310	62.5	5.2	443	2	F30010	1383	62.5	5.2	305	2	T43972	hypothetical prote
1311	62.5	5.2	443	2	T08136	1384	62.5	5.2	306	2	A10209	probable sugar ABC
1312	62.5	5.2	443	2	G64844	1385	62.5	5.2	306	2	T41290	conserved hypochet
1313	62.5	5.2	452	2	G85647	1386	62.5	5.2	312	2	S48851	chalcone reductase
1314	62.5	5.2	452	2	G90787	1387	62.5	5.2	312	2	S48849	hypothetical prote
1315	62.5	5.2	455	2	D97217	1388	62.5	5.2	315	2	T24821	hypothetical prote
1316	62.5	5.2	457	2	P69662	1389	62.5	5.2	331	2	AB3117	hypothetical prote
1317	62.5	5.2	459	2	AF3284	1390	62.5	5.2	344	2	T05987	hypothetical prote
1318	62.5	5.2	461	2	S57713	1391	62.5	5.2	345	2	T32203	hypothetical prote
1319	62.5	5.2	468	2	A49131	1392	62.5	5.2	351	2	C86408	F3H9.12 protein -
1320	62.5	5.2	470	2	C70641	1393	62.5	5.2	352	2	C98170	hypothetical prote
1321	62.5	5.2	487	2	S73161	1394	62.5	5.2	353	2	T42971	hypothetical prote
1322	62.5	5.2	490	2	T40116	1395	62.5	5.2	360	2	A53611	interleukin-8 rece
1323	62.5	5.2	492	2	AC0768	1396	62.5	5.2	360	2	T33260	hypothetical prote
1324	62.5	5.2	494	2	T15502	1397	62.5	5.2	362	2	B57641	G protein-coupled
1325	62.5	5.2	501	1	CN0539	1398	62.5	5.2	363	2	S42379	hypothetical prote
1326	62.5	5.2	502	2	C86263	1399	62.5	5.2	370	2	H84111	response regulator
1327	62.5	5.2	505	2	S44647	1400	62.5	5.2	377	2	T05427	hypothetical prote
1328	62.5	5.2	507	2	S52677	1401	62.5	5.2	379	2	S58457	ubiquinol-cytochro
1329	62.5	5.2	546	2	AE0571	1402	62.5	5.2	379	2	E58851	ubiquinol-cytochro
1330	62.5	5.2	547	2	S64332	1403	62.5	5.2	381	2	T11440	probable two-compo
1331	62.5	5.2	548	2	S64567	1404	62.5	5.2	383	2	C95965	bicyclomycin resis
1332	62.5	5.2	559	2	T22928	1405	62.5	5.2	398	1	E64112	hypothetical prote
1333	62.5	5.2	572	2	T11478	1406	62.5	5.2	399	2	F72417	translocation prot
1334	62.5	5.2	578	2	I56215	1407	62.5	5.2	399	2	JC5879	cell-division prot
1335	62.5	5.2	580	2	T02596	1408	62.5	5.2	402	2	D70186	xylose operon regu
1336	62.5	5.2	601	2	T11451	1409	62.5	5.2	402	2	B69338	conserved hypochet
1337	62.5	5.2	608	2	T34391	1410	62.5	5.2	403	2	H72084	cbs domain protein
1338	62.5	5.2	610	2	A28798	1411	62.5	5.2	411	2	H72084	protein-tyrosine-P
1339	62.5	5.2	621	2	B95897	1412	62.5	5.2	432	1	A34845	hypothetical prote
1340	62.5	5.2	638	2	G02068	1413	62.5	5.2	432	2	T21880	hypothetical prote
1341	62.5	5.2	668	2	C71868	1414	62.5	5.2	435	2	T47737	hypothetical prote
1342	62.5	5.2	685	2	T04073	1415	62.5	5.2	444	2	F81367	probable transmemb
1343	62.5	5.2	697	2	T19254	1416	62.5	5.2	454	2	H65054	hypothetical prote



1417	62	5.2	458	2	A84487	probable replicati
1418	62	5.2	466	2	AH1800	transmembrane effi
1419	62	5.2	474	2	E64232	hypothetical prote
1420	62	5.2	483	2	E46124	nuclear protein EN
1421	62	5.2	487	2	T05271	probable 3-oxoacyl
1422	62	5.2	497	1	S53834	NADH2 dehydrogenas
1423	62	5.2	497	2	S66834	probable membrane
1424	62	5.2	499	2	B81914	probable periplasm
1425	62	5.2	502	2	A82372	hypothetical prote
1426	62	5.2	514	2	A96671	ammonium transport
1427	62	5.2	528	1	ACCH2N	nicotinic acetylch
1428	62	5.2	555	2	T08869	protein P2 - Acyrt
1429	62	5.2	567	2	S29498	lymphocyte antigen
1430	62	5.2	582	2	S19424	hypothetical prote
1431	62	5.2	585	2	T02360	hypothetical prote
1432	62	5.2	600	2	H98149	ATP-binding transp
1433	62	5.2	600	2	AD3138	hypothetical prote
1434	62	5.2	630	2	H83686	PTS system, beta-g
1435	62	5.2	644	2	T20034	hypothetical prote
1436	62	5.2	660	2	A44432	amino acid transpo
1437	62	5.2	667	2	T20799	hypothetical prote
1438	62	5.2	675	1	S46952	phosphotransferase
1439	62	5.2	675	2	T20822	hypothetical prote
1440	62	5.2	678	2	F71921	hypothetical prote
1441	62	5.2	702	2	T03903	hypothetical prote
1442	62	5.2	707	2	A35804	nucleolin - human
1443	62	5.2	724	1	HMS84	heat shock protein
1444	62	5.2	739	2	T25030	hypothetical prote
1445	62	5.2	743	2	A29232	101k malaria antig
1446	62	5.2	750	2	S73829	probable ABC trans
1447	62	5.2	756	2	A88679	protein H06H21.10
1448	62	5.2	791	2	A46616	cytochrome-c oxida
1449	62	5.2	810	1	A33380	interleukin-4 rece
1450	62	5.2	841	2	T09455	vacuolar assembly
1451	62	5.2	848	2	E95092	aminopeptidase N
1452	62	5.2	864	2	T42556	regument protein 1
1453	62	5.2	872	1	TNBEH	97k alpha trans-in
1454	62	5.2	911	2	S70958	ORNA protein - Vib
1455	62	5.2	932	2	C70191	penicillin-binding
1456	62	5.2	950	1	PMBYR1	Ca2+-transporting
1457	62	5.2	1002	2	G97217	conserved membrane
1458	62	5.2	1024	2	A83557	acriiflavin resista
1459	62	5.2	1030	2	T13153	Rab6 GTPase activa
1460	62	5.2	1031	2	T43458	hypothetical prote
1461	62	5.2	1041	2	T29010	hypothetical prote
1462	62	5.2	1242	2	G88480	protein C16A3.7 [i
1463	62	5.2	1273	2	C96767	unknown protein F2
1464	62	5.2	1283	2	T18939	hypothetical prote
1465	62	5.2	1321	2	A60165	sodium channel pro
1466	62	5.2	1380	2	T20695	hypothetical prote
1467	62	5.2	1802	2	T33783	bactitracin synthe
1468	62	5.2	6359	2	T31679	hypothetical prote
1469	62	5.2	99	2	B99233	hypothetical prote
1470	61.5	5.1	134	2	E69985	hypothetical prote
1471	61.5	5.1	149	2	C86855	hypothetical prote
1472	61.5	5.1	150	2	S43955	probable NADH2 de
1473	61.5	5.1	159	2	S77185	hypothetical prote
1474	61.5	5.1	162	2	A72618	lipoprotein signal
1475	61.5	5.1	162	2	E97400	hypothetical prote
1476	61.5	5.1	163	2	J55045	epithelial membran
1477	61.5	5.1	173	2	H97775	hypothetical prote
1478	61.5	5.1	176	2	G89947	hypothetical prote
1479	61.5	5.1	176	2	S40726	hypothetical prote
1480	61.5	5.1	183	2	H70478	hypothetical prote
1481	61.5	5.1	185	2	H69377	conserved hypotnet
1482	61.5	5.1	190	2	A26630	nucleoplasm A -
1483	61.5	5.1	212	2	A83521	conserved hypotnet
1484	61.5	5.1	225	2	T19811	hypothetical prote
1485	61.5	5.1	264	2	T18998	hypothetical prote
1486	61.5	5.1	272	2	G82888	hypothetical prote
1487	61.5	5.1	273	2	T28980	hypothetical prote
1488	61.5	5.1	274	2	S42168	NADH2 dehydrogenas
1489	61.5	5.1	276	2	F72342	conserved hypotnet

1490	61.5	5.1	278	2	D83080	hypothetical prote
1491	61.5	5.1	279	2	AG0421	sugar transport sy
1492	61.5	5.1	284	2	AC3429	peroxamine synthet
1493	61.5	5.1	289	2	F91269	hypothetical prote
1494	61.5	5.1	289	2	D86110	hypothetical prote
1495	61.5	5.1	290	2	AE0947	ribonuclease BN (E
1496	61.5	5.1	292	2	AE1539	sugar ABC transport
1497	61.5	5.1	293	2	C90032	hypothetical prote
1498	61.5	5.1	293	2	A83710	ABC transporter (p
1499	61.5	5.1	293	2	B69866	transcription regu
1500	61.5	5.1	294	2	AD0886	probable oxidoredu

## ALIGNMENTS

RESULT 1  
 MLN 64 protein - human  
 C:Species: Homo sapiens (man)  
 C>Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
 C:Accession: I38027; S60682  
 R:Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chenard, M.P.; Lidereau, R.  
 Genomics 28, 367-376, 1995  
 A>Title: Identification of four novel human genes amplified and overexpressed in breast  
 A:Reference number: I37080; MUID:96039245; PMID:7490069  
 A:Accession: I38027  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-445 <RES>  
 A:Cross-references: UNIPROT:Q14849; UNIPARC:UPI000012P1BC; EMBL:X80198; NID:G951278; PIDK  
 A>Note: submitted to the EMBL Data Library, July 1994  
 C:Genetics:  
 A:Gene: MLN64

Query Match 55.6%; Score 664; DB 2; Length 445;  
 Best Local Similarity 56.2%; Pred. No. 8, 7e-55;  
 Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

QY	1	MNHLP-----EDMENAL-----TSSQSHASLRNHSINPTQLMARLESYGRKKGISDV 51	
DB	1	MSKLPRELTRDLRRSLPAVASLSLSHQSLSHLPPPE-----KRAAISDV 49	

QY	52	RRFRFCFVTPDLLFVTLMIIEANWNGIENTLEKEMVDYSSVFDFLLAVFRKVL 111	
DB	50	RRFRFCFVTPDLLFISLMIIEINTMTGIRKMLEOBIIOYFKTSFDFVLAFFRSG 109	

QY	112	ILAYAVCRLRHWMAIALTTAVTSAPFLAKYILSKLSQCAFQGVLPPIISFILAMIEI 171	
DB	110	LLGAYAVQLRHWMAIVATTVSSAFILVKYILSELKGAFGILPLVSVLAMEITWFL 169	

QY	172	DFKVLPOEAEEENRLILVQDASERAAI-L-PGSLSDGQFVSPPESEAGSE-EAEKKDSEK 229	
DB	170	DFKVLPOEAEEENRWYLAQAVARGPILFFGALSEGFFVSPPESEAGSDNESDEAVGKK 229	

RESULT 2  
 T16170  
 hypothetical protein F26F4.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: T16170  
 R:Fulton, L.  
 submitted to the EMBL Data Library, March 1996  
 A:Description: The sequence of C. elegans cosmid F26F4.  
 A:Reference number: Z18471  
 A:Accession: T16170  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-478 <FUL>  
 A:Cross-references: UNIPROT:Q19819; UNIPARC:UPI000017B938; EMBL:U12964; NID:G1213452; PII  
 A:Experimental source: strain Bristol N2  
 C:Genetics:

A:Gene: CBSP.F26P4.4  
A:Introns: 47/2; 81/2; 125/3; 171/3; 214/1; 236/2; 343/3; 444/1

Query Match 17.1%; Score 204; DB 2; Length 478;  
Best Local Similarity 26.5%; Pred. No. 2.5e-11;  
Matches 56; Conservative 36; Mismatches 73; Indels 46; Gaps 6;

QY 42 GREKKGISDVRRCFCLEVFEDLLFVTLMI-----ELNVNGIENTLEK 86  
DB 69 GSGRIGVSKRKRFFVTFPDTSTILLMLCTYTRDDMDKVFENLNI-----FNP 121

QY 87 EVNQYDYSSYFDIFLLAVFRFKVLLAYAVCRLRHMAIALTTAVTSAPLLAKVLSKL 146  
DB 122 KFLRI-----SLFPIVLLAVLRMLIGVYGCIVKQVYVAFTTLASSAYIMKVLFPYN 177

QY 147 FSGGAGFYVPLII-SFLIAMIETWFLDKVLPQAEENRLLIYQDASERAAALIPGSLD 205  
DB 178 HSSSAVFPFLIIITSFLLCMSEFYLMFPOLFRERYARREL-----DGLEN 224

QY 206 GQFYSPPESEA-----GSEAEKQDSEKP 230  
DB 225 PEFSTDEARSNRHRGRQNSGNSCAP 255

RESULT 3  
H90281  
hypothetical protein dppB-1 [imported] - Sulfolobus solfataricus  
C/Species: Sulfolobus solfataricus  
C/Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C/Accession: H90281

R;Sheng, Q.; Shingh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.  
submitted to Genbank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: H90281  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-348 <KUR>  
A:Cross-references: UNIPROT:Q97YQ0; UNIPARC:UPI00000643D5; GB:AE006641; NID:g13814471; F  
C:Genetics:  
A:Gene: dppB-1

Query Match 8.6%; Score 102.5; DB 2; Length 348;  
Best Local Similarity 23.7%; Pred. No. 0.064;  
Matches 49; Conservative 35; Mismatches 66; Indels 57; Gaps 9;

QY 15 SOSSHASLRNHSINPTQLMARISYEGREKKGISDVRRCFCLEVFEDLLFVTLMIIEEL 74  
DB 46 AOPSQTLFKAHNHNSTQIQIAVEKY--RE-----SLIAVGL 81

QY 75 NVNGGIENTLEK-----EVNQYDYSSYFDIFLLAVFRFKVLLAYAVCRLRHMAIAL 128  
DB 82 N-----QPIIDKYFIQWYNNLMRPFQGTAYF-LQAPSGREVSIIAYLPR-----TILL 130

QY 129 TTAVTASFLAKVLSKLFSGAGF-GYVLPILISFLIAMIETWFLDKVLPQAEENRLL 187  
DB 131 FTTATVFIIVAGTIIIGLSAKSKFWEKVIATIAVHSSIPTWMLGF-----VL 178

QY 188 IYQDASERAAALIPGSLDQGFYSPES 214  
DB 179 IAAIAYAVKVPFPGGKTS---VPPPKN 202

RESULT 4  
D75080  
glucose-1-phosphate thymidyltransferase related protein PAB2433 - Pyrococcus abyssi (E  
C/Species: Pyrococcus abyssi  
C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: D75080  
R;anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc  
A:Reference number: A75001  
A:Accession: D75080  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-424 <KAM>  
A:Cross-references: UNIPROT:Q9UZM1; UNIPARC:UPI000003471C; GB:AJ248286; GB:AL096836; NID  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB2433  
C:Superfamily: Aquifex aeolicus glucose-1-phosphate thymidyltransferase

Query Match 7.8%; Score 93.5; DB 2; Length 424;  
Best Local Similarity 21.9%; Pred. No. 0.57;  
Matches 47; Conservative 25; Mismatches 72; Indels 71; Gaps 7;

QY 5 PEDMENA-----LTGSQSHASLRNHSINPTQLMARISYEGRE 44  
DB 207 PEDIKKARKLIVYTSVKGVDGPFISRHLNRKISTRISALVHEVTPNQ----- 255

QY 45 KKGISDVRRCFCLEVFEDLLFVTLMIIELVNG-----GIENTLEKEVMQYDY 93  
DB 256 -----TIVTLPGLFISALMNFISVPIAGILYQVSSIDGVDGEIARARMQISK 303

QY 94 YSSYFDIFLLAVFRFK-VLLAYAVCRLRHMAIALTTAVTSAPL-----L 138  
DB 304 FCGYFDSLDRYVDFFTLLIAYVSIREDPLWMAIALAMFSANVSYSTERFKAGVCYDA 363

QY 139 AKVF--LSKLFSGAGFYVPLIISFLIAMIETWFL 171  
DB 364 YKVIPALRKVPGRKDERIFLTMLLTLVGMVKAFL 398

RESULT 5  
T43048  
calcium channel alpha-1 chain - Cyanea capillata  
C/Species: Cyanea capillata  
C/Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C/Accession: T43048

R;Jezioriski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V.  
U. Biol. Chem. 273, 22792-22799, 1998  
A:Title: Cloning and functional expression of a voltage-gated calcium channel alpha sub  
A:Reference number: 222300; MUID:98380510; PMID:9712913  
A:Accession: T43048  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1911 <JEZ>  
A:Cross-references: UNIPROT:O02038; UNIPARC:UPI000007C488; EMBL:U93075; NID:g1947095; PII  
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain  
C:Keywords: transmembrane protein

Query Match 7.5%; Score 90; DB 2; Length 1911;  
Best Local Similarity 23.5%; Pred. No. 7.2;  
Matches 43; Conservative 33; Mismatches 59; Indels 48; Gaps 9;

QY 5 PEDMENALTSQSSHASLRNHSINPTQLM-----ARISYEGREKKGISDV----- 51  
DB 791 PEDVE--LGNKSKNGKTRHNGETTSTMSGKARIFPLALSELNLIKDIIDPMPRESS 848

QY 52 -----RRTFCLFVTFEDLLFVT--LWIIELNVNGGIENTLEKEVMQYDYSSYFDI 100  
DB 849 FFIISANKRLAYLCYRLAVNKFINSILVLIIMSSVALAABDPGRDYLK-NKILGYFDI 907

QY 101 FLAVFRKVLII-LAYAV-----CR-----LRHMAIALTT-AVTSAPFLA 139  
DB 908 FETAMFTEVTKMIAFGVILHKRSFCRSFENQDLVIVAVSWAATMLSRGSAISVRI 967

QY 140 KVI 142  
DB 968 RVL 970

RESULT 6



QY 98 FDIPLAVRFKVLILAVACRLRHMAIALTTAVTSAPILAKVI--LSKLFSGA----- 151  
Db 331 LHSFVLPIFSFPAVPIFYTL-KYSHLIGITLRYSVSAPFPAALAFQYLFQGFPAASPSF 389  
QY 152 -----FGVVLPIISFILAMIEFWLDFKVLPOEAEENRLIIV-----OPASERAA 197  
Db 390 GAIMEGSVFPEVYITIP-IAFVLA-----NYTNLPFE-----IIVFIPSLDPAIKLVV 434  
QY 198 LIPGGLSDGOFYS 210  
Db 435 SLP-----YFYS 441

## RESULT 10

A41680  
Integral membrane protein ppsa - Chinese hamster  
C:Species: Citicellus griseus (Chinese hamster)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 06-Oct-2000  
C:Accession: A41680  
R:Kuge, O.; Nishijima, M.; Akamatsu, Y.  
J. Biol. Chem. 266, 24184-24189, 1991  
A:Title: A Chinese hamster cDNA encoding a protein essential for phosphatidylserine synthase  
A:Reference number: A41680; MUID:32084729; PMID:1748687  
A:Accession: A41680  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-471 <KUG>  
A:Cross-references: UNIPARC:UPI000013280F; GB:D10234; GB:D90468; NID:g220280; PIDN:BA01  
C:Superfamily: Caenorhabditis elegans hypothetical protein ZC506.3  
C:Keywords: membrane protein

Query Match 7.1%; Score 84.5; DB 2; Length 471;

Best Local Similarity 24.4%; Pred. No. 4.6;

Matches 32; Conservative 22; Mismatches 38; Indels 39; Gaps 7;

QY 55 FCLFVTFDLFVTLMIETLVNNGIENLEKEVMOY-----DYSSYDFDIFLAV 105  
Db 117 FLFLFNFQYKSLMYW-LDENLRYA---TREADIMEYAVNCHVTWERYSHFIDIFAFGH 172  
QY 106 F---REKVLILAVACRLRHMAIALTTAVTSAPILAKVILSKLFSQAGFVVLPIISF 161  
Db 173 FVGWAMKALLIRSYGLC-----WTISITWELTELF-----FMHLLP--NF 210  
QY 162 ILAMIEFWL 172  
Db 211 AECWMDQVILD 221

## RESULT 11

H97002  
probable integral membrane protein (imported) - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: H97002  
R:Rolling, J.; Bretton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: H97002  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-352 <KUR>  
A:Cross-references: UNIPROT:Q97KTI; UNIPARC:UPI0000009CF; GB:AE001437; PIDN:AAK78811.1;  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC0835

Query Match 7.0%; Score 83.5; DB 2; Length 352;  
Best Local Similarity 19.2%; Pred. No. 4.1;  
Matches 38; Conservative 35; Mismatches 50; Indels 75; Gaps 8;

QY 38 ESEYREKGISDVRRTECFLEVTED-----LLFVTLMIETL 74  
Db 115 EFNVVRDKTNEDMKLIKAVLVQNTLMNERIVKDEQIGLSKSERIIFLAVTLITS 174  
QY 75 NVNGGI-----ENTLEKEVMO-----YVYSSYPDIF-----LAVFRKVL 111  
Db 175 VNGAVVIRDRRENTYVRKVSNSKPEYFGVNYVYISYQLFANSIMAFGLIYG 234  
QY 112 I-----LAVAVCRRLRHMAIALTTAVTSAP-----LLAKVILSKLFSQAGFVVLPIIS 160  
Db 235 ISFLKMLSYGL-----ILTVWTTGTFIVCFNKELVAMRMSAA-----IS 276  
QY 161 FILAMIEFWLDFKVLPO 178  
Db 277 LILSLVGTFINXKIME 294

## RESULT 12

AE0302  
sugar ABC transporter, permease protein YPO2476 (imported) - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AE0302  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchell, R.W.; Holden, M.T.G.; Prentice, M.B.;  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, F.  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AE0302  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-291 <KUR>  
A:Cross-references: UNIPROT:Q8ZDT0; UNIPARC:UPI00000DCC19; GB:AL590842; PIDN:CAC91281.1;  
C:Genetics:  
A:Gene: YPO2476  
C:Superfamily: inner membrane protein uspa

Query Match 6.9%; Score 83; DB 2; Length 291;

Best Local Similarity 22.3%; Pred. No. 3.6;

Matches 44; Conservative 26; Mismatches 57; Indels 70; Gaps 10;

QY 46 KGISDVRRTECFVTFDLFVTLMIETLVN-----GGIENL----- 84  
Db 9 KQVGSVLAASYLGYSIFWFYPIWLAVLSIEWRFVGIPTFNGLNPFILWQDPLFWKS 68  
QY 85 EKEVMQDYSSYFDIFLAVFRKVLILAVACRLRHMAIALTTAVTSAPILAKV--- 141  
Db 69 MLNVMRFLMY--YLPVIFISSFLF-----AFGLQKLXHG-----RTFVALSFLIANVSSG 116  
QY 142 -----LSKLFSGA-----FGVVLPIIS-----FILAMIEFW-----FL 171  
Db 117 VAVSVSKLFSQGNPLNTFLYDFGFTLPWLTSPDPMASIALVWVMKFGYGLIIFS 176  
QY 172 DFKVLPOE---AEEN 184  
Db 177 GLNSIPKEIYSABELDN 193

## RESULT 13

S34960  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrion  
C:Species: mitochondrion Crithidia oncopelti  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S34960  
R:Maiov, D.A.; Horvath, A.; Guang II, K.; Kolesnikov, A.A.  
submitted to the EMBL Data Library, October 1990  
A:Reference number: S34958  
A:Accession: S34960  
A:Molecule type: DNA  
A:Residues: 1-590 <MAS>  
A:Cross-references: UNIPROT:Q34192; UNIPARC:UPI000008E400; EMBL:X56015; NID:g12879; PIDN

Query Match 7.0%; Score 83.5; DB 2; Length 352;  
Best Local Similarity 19.2%; Pred. No. 4.1;  
Matches 38; Conservative 35; Mismatches 50; Indels 75; Gaps 8;

A:Gene: NDS  
A:Genome: mitochondrion  
A:Genetic code: SGC6

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.9%; Score 83; DB 1; Length 590;

Best Local Similarity 23.9%; Pred. No. 8.3; Mismatches 37; Indels 42; Gaps 7;

Matches 32; Conservative 23; Mismatches 37; Indels 42; Gaps 7;

QY 55 FCLFVPT-----DL-----FVTLMIIELVNGIGIENTLEKEVMQDYSSYFDIFLLAVP 106

Db 95 FILFAYAYWYDMLKRFNIFWVFLCMVFF-----LSYDLTAACGWEILGLF 146

QY 107 RFKVLIAVAVCRLRHWMALATTAVTSAPFLAVIISKLFSGAGFGVLPITISFILAWI 166

Db 147 SF--FLISY-----FWYRFPAKFGKSPFSIKI-----GDVLLLSFVMTFI 187

QY 167 ET-----WFLDF 173

Db 188 STGGMINFYFVN 201

#### RESULT 14

B29835 Tras protein - Escherichia coli plasmid PED208

C:Species: Escherichia coli  
C:Date: 04-Aug-1988 #sequence\_revision 04-Aug-1988 #text\_change 09-Jul-2004

C:Accession: B29835

R:Finlay, B.B.; Paranchych, W.  
J. Bacteriol. 166: 713-721, 1986

A:Title: Nucleotide sequence of the surface exclusion genes tras and trat from the IncF-

A:Reference number: A29835; MUID:8623783; PMID:3011738

A:Accession: B29835

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-186 <FIN>

A:Cross-references: UNIPROT:P14498; UNIPARC:UPI0000001563

C:Genetics:

A:Genome: plasmid

Query Match 6.9%; Score 82.5; DB 2; Length 186;

Best Local Similarity 23.8%; Pred. No. 2.4; Mismatches 40; Indels 35; Gaps 6;

Matches 31; Conservative 24; Mismatches 40; Indels 35; Gaps 6;

QY 61 FDLFVTLMIIELVNGIGIENTLEKEVMQDYSSYFDIFL-----AVRFKVLILAY 115

Db 44 FQLLFI-----IFDLFINSNR-----DYH--YFDTEVITLGSNAFSLVFLMSTY 87

QY 116 AVCRLRHWMALATTAVTSAPFLAVIISKLFSGAGFGVLPIT-----SFLIAW 165

Db 88 NLVSLK-----ISLSEITEQSVLKLVERKINSYGOFLMVNAIVGCVLLSSGERFVAGL 143

QY 166 IETWFLDFKV 175

Db 144 GFSMFVTYLI 153

#### RESULT 15

C64227 hypothetical protein homolog MG247 - Mycoplasma genitalium

C:Species: Mycoplasma genitalium  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: C64227

R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J. C.A.; Venter, J.C.  
Science 270: 397-403, 1995

A:Title: The minimal gene complement of Mycoplasma genitalium.  
A:Reference number: A64200; MUID:96026346; PMID:756993

A:Accession: C64227

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-239 <TIGR>

A:Cross-references: UNIPROT:P47489; UNIPARC:UPI00001394F7; GB:U39703; GB:L43967; NID:G384

A:Experimental source: strain G-37

C:Genetics:

A:Genetic code: SGC3

C:Superfamily: Escherichia coli ygiH protein

Query Match 6.9%; Score 82.5; DB 1; Length 239;

Best Local Similarity 21.7%; Pred. No. 3.2; Mismatches 54; Indels 39; Gaps 8;

Matches 33; Conservative 26; Mismatches 54; Indels 39; Gaps 8;

QY 42 GREKGISDVRRTF-----CLFVFDLLFVTL--WIELVNGIGIENTLEKEVMQYD 92

Db 42 GSKNPGATNSMRVFGKIGFLVAIPDAFKGFALFTWIL--FRFGLQGYTEKYOST 98

QY 93 YSSSYFDIFLLAY-----FRK---VILLAVAVCRLRHWMAL-----ALTAVTSA 135

Db 99 YFLSYLSCFAATIGHIFPLFYKFGKGAATGSGLSAISLWMLCLLIIMITLITKY 158

QY 136 FILAKVLSKLFSGAGFGVLPITISFILAWIE 167

Db 159 VSLASLITF-----FVLAVI--IIPWLD 180

Search completed: May 12, 2006, 20:44:15  
Job time : 82 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 12, 2006, 20:38:52 ; Search time 228 Seconds  
(without alignments)  
724.095 Million cell updates/sec

Title: US-10-063-518-14

Perfect score: 1195  
Sequence: 1 MNHLPEMDENALTGSSQSHA.....EAGSEAEKXDEKPLELL 234

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1500 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1195	100.0	234	1 MENTO_HUMAN	O95772 homo sapien
2	1141.5	95.5	235	2 O5U205_RAT	O5U205 rattus norv
3	1134.5	94.9	235	1 MENTO_MOUSE	O96C13 mus musculus
4	796	66.6	227	2 O6D138_BRARE	O6D138 brachydario
5	700.5	58.6	448	2 O6DFP7_XENTR	O6DFP7 xenopus tro
6	698.5	58.5	444	2 O6PP40_XENLA	O6PP40 xenopus lae
7	684	57.2	448	2 O6GNT3_XENLA	O6GNT3 xenopus lae
8	664	55.6	445	1 MLN64_HUMAN	O6GNT3 xenopus lae
9	664	55.6	445	2 O53Y53_HUMAN	O53Y53 homo sapien
10	656.5	54.9	446	1 MLN64_MOUSE	O61542 mus musculus
11	656.5	54.9	446	2 O5U2T5_RAT	O5U2T5 rattus norv
12	656.5	54.9	446	2 O544C3_MOUSE	O544C3 mus musculus
13	632	52.9	448	1 MLN64_BRARE	O96f54 brachydario
14	586.5	49.1	501	2 OAS943_TETNG	O96f43 letriodon n
15	566	47.4	501	2 OAS970_PONPY	O5Bd70 pongo pygma
16	492	41.2	107	2 O8BMP8_MOUSE	O8BMP8 m mus muscu
17	364.5	30.5	574	2 O563D1_AEDAE	O563d1 aedes aegypt
18	364.5	30.5	595	2 O563D1_AEDAE	O563d0 aedes aegypt
19	346	29.0	523	2 O7QIT3_ANOGA	O7QIT3 anopheles g
20	343	28.7	545	2 O8MZ14_DROME	O8MZ14 drosophila
21	343	28.7	583	2 O9W145_DROME	O9W145 drosophila
22	342.5	28.7	131	2 O4THH5_TETNG	O4thh5 tetraodon n
23	272	22.8	197	2 O4SNJ2_TETNG	O4snj2 tetraodon n
24	206.5	17.3	419	2 O6OZ70_CABBR	O6OZ70 caenorhabdi
25	204	17.1	447	2 O19819_CABBR	O19819 caenorhabdi
26	181.5	15.2	141	2 O4SNJ3_TETNG	O4snj3 tetraodon n
27	104.5	8.7	294	1 MLN64_SALFO	O90Zb9 salvelinus
28	102.5	8.6	348	2 O97YQ0_SULISO	O97YQ0 sulfolobus
29	99.5	8.3	1095	2 O4W7C1_THEPA	O4W7C1 thelloeria p
30	96.5	8.1	714	2 O5LPT4_STIPO	O5LPT4 salicibacte
31	93.5	7.8	424	2 O9UZWI_PYRAB	O9UZWI pyrococcus

32	93.5	7.8	438	1 CLN3_MACPA	O60h0 macaca fasc
33	93.5	7.6	564	2 O8H010_THRIM	O8h010 thrips imag
34	91	7.6	246	2 O8DU10_STRMU	O8du10 streptococc
35	91	7.6	525	2 O7VFT4_HELHP	O7vft4 helicobacte
36	91	7.6	651	2 O8DZX0_STRAS	O8dZX0 streptococc
37	91	7.6	651	2 O8ESM0_STRAS	O8eSM0 streptococc
38	90.5	7.6	262	2 O7NBJ4_MYCGA	O7nbj4 mycoplasma
39	90.5	7.6	530	2 O54R03_DICDI	O54f03 dictyostell
40	90	7.5	1911	2 O02038_CYACP	O02038 cyanea capi
41	89.5	7.5	233	2 O6UCT3_9HEMI	O6uct3 aleurodictus
42	89.5	7.5	367	2 O8HEH8_9ACAR	O8eh8 varroa dest
43	89.5	7.5	376	2 O6UCT6_9HEMI	O6uct6 aleurodictus
44	89.5	7.5	478	2 O60INO_CABBR	O60ino caenorhabdi
45	89.5	7.5	488	2 O840W7_STIMU	O840w7 streptococc
46	89	7.4	373	2 O7RTB5_PLAYO	O7rtb5 plasmodium
47	89	7.4	387	2 O56BR5_BRARE	O56br5 brachydario
48	89	7.4	897	2 O5K830_CRYHE	O5K830 cryptococcu
49	89	7.4	912	2 O4YCI1_PLABE	O4yci1 plasmodium
50	88.5	7.4	384	2 O6NMV4_RANCA	O6nmv4 rana catesb
51	88.5	7.4	755	2 O60OU6_CABBR	O60ou6 caenorhabdi
52	87.5	7.3	336	2 O4HDY8_CAMCO	O4hdy8 campylobact
53	87.5	7.3	473	2 O5ZM65_CHICK	O5zme5 gallus gall
54	87	7.3	304	2 O640E5_XENLA	O640e5 xenopus lae
55	87	7.3	610	2 O7RRS2_PLAYO	O7rrs2 plasmodium
56	87	7.3	707	2 O6GN42_XENLA	O6gn42 xenopus lae
57	87	7.3	720	2 O8PYM2_METMA	O8pym2 methanosarc
58	87	7.3	766	2 O55IU0_CRYHE	O55iu0 cryptococcu
59	86.5	7.2	328	2 O7NUL9_GLOVT	O7n19 gloebacter
60	86.5	7.2	626	2 O7Z205_CABEL	O7z205 caenorhabdi
61	86.5	7.2	647	2 O4Y844_PLABE	O4y844 plasmodium
62	86.5	7.2	891	2 O81LA2_9POXY	O81la2 ectromella
63	86	7.2	1050	2 O871G6_NEURC	O871g6 neurospora
64	86	7.2	1056	2 O757L6_NEURC	O757l6 neurospora
65	86	7.2	1453	2 O4PAR7_USTWA	O4par7 usiliago ma
66	86	7.2	2515	2 O4S220_TETNG	O4s220 tetraodon n
67	85.5	7.2	174	2 P97067_9ENTR	P97067 salmonella
68	85.5	7.2	336	2 O95086_HUMAN	O95086 homo sapien
69	85.5	7.2	337	2 O4Y634_PLACH	O4y634 plasmodium
70	85.5	7.2	339	2 O95089_HUMAN	O95089 homo sapien
71	85.5	7.2	336	2 O9PMES_CAMJE	O9pmes campylobact
72	85.5	7.2	438	1 CLN3_HUMAN	O1326 homo sapien
73	85.5	7.2	438	2 O549S9_HUMAN	O549s9 homo sapien
74	85.5	7.2	473	1 PTSS1_HUMAN	P4861 homo sapien
75	85.5	7.2	747	2 O93GL8_SALTU	O93gl8 salmonella
76	85	7.1	348	2 O9SE17_ARATH	O9se17 arabidopsis
77	85	7.1	377	2 O612C1_BACAN	O612c1 bacillus an
78	85	7.1	448	2 O51531_BORBU	O51531 borrelia bu
79	85	7.1	797	2 O82GJ8_STRAM	O82gj8 streptomyce
80	84.5	7.1	412	2 O4ITL6_AZOVY	O4itl6 azotobacter
81	84.5	7.1	430	2 O5ZTB7_LEGPH	O5ztb7 legionella
82	84.5	7.1	471	1 PTSS1_CRIGR	O005f6 cricetulus
83	84.5	7.1	473	2 O5A9S9_HUMAN	O5a9s9 mus musculu
84	84.5	7.1	473	2 O5POJ5_RAT	O5pjl5 rattus norv
85	84.5	7.1	487	2 O6A0B5_MOUSE	O6a0b5 mus musculu
86	84.5	7.1	892	2 O9JP90_VACCT	O9jfp90 vaccinia vi
87	84.5	7.1	1118	2 O65U88_MANGM	O65u88 manheimia
88	84.5	7.1	3848	2 O5CUD5_CRYTV	O5cus5 crytospori
89	84	7.0	396	2 O5HSK1_CAMAR	O5hsr1 campylobact
90	84	7.0	469	2 O9HUK8_THEAC	O9h8r thermoplasma
91	84	7.0	493	2 O7TSJ1_MOUSE	O7tsj1 mus musculu
92	84	7.0	1700	2 O75JN1_DICDI	O75jn1 dictyostell
93	83.5	7.0	275	2 O4Y932_PLABE	O4y932 plasmodium
94	83.5	7.0	303	2 O6FNB8_CANGA	O6fn8 candida gla
95	83.5	7.0	322	2 O8LB40_ARATH	O8lb40 arabidopsis
96	83.5	7.0	352	2 O97KT1_CLOAB	O97kt1 clostridium
97	83.5	7.0	352	2 O6K124_MYCOW	O6k124 mycoplasma
98	83.5	7.0	380	2 O97C55_THEVO	O97c55 thermoplasma
99	83.5	7.0	429	2 O5B5F1_VYBPI	O5b5f1 vibrio fisc
100	83.5	7.0	490	2 O9CTA9_MOUSE	O9cta9 mus musculu
101	83.5	7.0	599	2 O6PCX2_MOUSE	O6pcx2 mus musculu
102	83.5	7.0	662	2 O88P20_PSEPK	O88p20 pseudomonas
103	83.5	7.0	834	2 O9JHFS_MOUSE	O9jht5 mus musculu
104	83.5	7.0	834	2 O9JHFS_MOUSE	O9jht5 mus musculu

105	83.5	7.0	834	2	09JL12_MOUSE	09JL12 mus musculus	178	81.5	6.8	645	2	067U09_ORYSA	067u9g oryza sativ
106	83.5	7.0	834	2	091W06_MOUSE	091w06 mus musculus	179	81.5	6.8	716	2	08DLB4_SYNE1	08dlb4 synchococc
107	83.5	7.0	1034	2	0722B9_TRYXR	0722b9 trypanosoma	180	81.5	6.8	735	2	06B3Y6_ECOLI	06b3y6 escherichia
108	83.5	7.0	2483	2	05CH29_CRYHO	05ch29 cryospori	181	81.5	6.8	892	2	0775R6_CAMPS	0775r6 camelpox vi
109	83	6.9	238	2	06YR96_ONYPE	06yr96 onion yello	182	81.5	6.8	892	2	08V2P5_CAMPM	08v2p5 camelpox vi
110	83	6.9	248	2	08GCS6_EUBAC	08gcs6 eubacterium	183	81.5	6.8	1092	2	0755K6_ASHGO	0755k6 ashya gose
111	83	6.9	221	2	08ZD70_YERPE	08zd70 yersteinia pe	184	81.5	6.8	1472	2	04SG06_TERNG	04sg06 tetraodon n
112	83	6.9	438	2	05XIH8_RAT	05xih8 rattus norv	185	81.5	6.8	1480	2	07R3B6_GIALA	07r3b6 giardia lam
113	83	6.9	589	2	07TMM1_MOUSE	07tmm1 mus musculus	186	81.5	6.8	1659	2	05KGP3_CRYNE	05kdp3 cryptococcu
114	83	6.9	590	2	034192_CRION	034192 crithidia o	187	81.5	6.8	1682	2	05S896_CRYNE	05s896 cryptococcu
115	83	6.9	1056	2	08C2V1_MOUSE	08c2v1 mus musculu	188	81	6.8	385	2	09Z069_ARATH	09z069 arabidopsis
116	83	6.9	1388	2	05DU28_MOUSE	05du28 mus musculu	189	81	6.8	480	2	06D043_ERWCT	06d043 erwina car
117	83	6.9	2661	2	07RMS4_PLAYO	07rms4 plasmodium	190	81	6.8	413	2	04MPN6_BACCE	04mpn6 bacillus ce
118	82.5	6.9	174	2	P97231_GENTR	P97231 salmonella	191	81	6.8	486	2	063ET7_BAC CZ	063et7 bacillus ce
119	82.5	6.9	166	1	TRAS21_ECOLI	P14498 escherichia	192	81	6.8	492	2	05A405_CANAL	05a405 candida alb
120	82.5	6.9	166	2	07BBW2_SALRT	Q7bbw2 salmonella	193	81	6.8	510	2	05ALJ4_CANAL	05alj4 candida alb
121	82.5	6.9	239	1	Y247_MYCGE	P47489 mycoplaema	194	81	6.8	520	1	Y0U1_CABEL	Y0u1 cabell
122	82.5	6.9	341	2	056918_YEREN	056918 yersteinia en	195	81	6.8	532	1	YHB7_YEAST	Yhb7 yeast
123	82.5	6.9	367	2	08HCK3_YACAR	08hck3 yarrowia dest	196	81	6.8	805	2	08XSV5_RALSO	08xsv5 ralsonia s
124	82.5	6.9	389	2	05FL80_LACAC	05fl80 lactobacill	197	81	6.8	1633	2	051NH6_MAGAR	051nh6 magnaporthe
125	82.5	6.9	406	2	087249_GLACT	087249 lactococcus	198	81	6.8	3010	2	08ORL8_9HEPC	08orl8 heparitis c
126	82.5	6.9	419	2	019134_RABIT	019134 oryctolagus	199	80.5	6.7	174	2	P97066_GENTR	08trne9 salmonella
127	82.5	6.9	471	2	09QW77_CRIGR	09qw77 cricetus	200	80.5	6.7	242	2	08TRN9_MERTAC	08trne9 metanosarc
128	82.5	6.9	510	2	0950M6_PFUNG	0950m6 rhizophyidiu	201	80.5	6.7	322	2	09SNE5_ARATH	09sne5 arabidopsis
129	82.5	6.9	604	2	08RHJ3_FUSNN	08rhj3 fusobacteri	202	80.5	6.7	322	2	056WV6_ARATH	056wv6 arabidopsis
130	82.5	6.9	717	1	TRADI_ECOLI	P09130 escherichia	203	80.5	6.7	353	1	MTRIA_PHOSU	P49217 phodopus su
131	82.5	6.9	781	2	04UEB8_THEAN	04ueb8 theileria a	204	80.5	6.7	366	2	086KR8_DICDI	086kr8 dicystostei
132	82.5	6.9	891	2	057223_PPOXY	057223 vaccinia vi	205	80.5	6.7	395	1	BTNI_SCHOU	09ue09 schizosacch
133	82.5	6.9	891	2	06J3A9_PPOXY	06j3a9 vaccinia vi	206	80.5	6.7	417	1	TNAB_PROVU	P28785 proteus vul
134	82.5	6.9	891	2	080MD2_COMPO	080md2 compox viru	207	80.5	6.7	423	2	04K1B8_STRPN	04k1b8 streptococc
135	82.5	6.9	892	2	06RZH3_PPOXY	06rzh3 rabdipox v	208	80.5	6.7	463	2	0722Q4_LISMF	0722q4 listeria mo
136	82.5	6.9	894	2	08OMU0_COMPO	08omu0 compox viru	209	80.5	6.7	463	2	08Y988_LISMO	08y988 listeria mo
137	82.5	6.9	1032	2	081501_LACBL	081501 lactobacill	210	80.5	6.7	463	2	05EAZ3_XENLA	05eaz3 xenopus lae
138	82.5	6.9	166	2	081501_PHEPC	081501 heparitis c	211	80.5	6.7	485	2	054Z56_DICDI	054z56 dicystostei
139	82	6.9	161	2	069UD2_ORYSA	069ud2 oryza sativ	212	80.5	6.7	486	2	09G861_9EUKA	09g861 malawimonas
140	82	6.9	228	2	05ESD8_VIBR1	05esd8 vibrio fisc	213	80.5	6.7	536	1	WVIN_CHLTR	046378 chlamydia t
141	82	6.9	301	2	08RLZ3_HAEIN	08rlz3 haemophilus	214	80.5	6.7	548	2	07RC45_PLAYO	07rc45 plasmodium
142	82	6.9	303	2	0818L8_HAEIN	0818l8 haemophilus	215	80.5	6.7	554	2	04Y6E4_PLACH	04y6e4 plasmodium
143	82	6.9	316	2	061RL6_CABER	061rl6 caenorhabdi	216	80.5	6.7	559	2	091ME6_PREOV	091me6 human rotav
144	82	6.9	382	2	050HS8_PORCI	050hs8 porphyromon	217	80.5	6.7	644	1	YNLS_YEAST	P53925 saccharomyc
145	82	6.9	384	2	050H01_PORGI	050h01 porphyromon	218	80.5	6.7	644	2	06B2V3_YEAST	06b2v3 saccharomyc
146	82	6.9	461	2	06AHB8_LEIXX	06ahb8 leishmania x	219	80.5	6.7	716	2	05UBP7_ECOLI	05ubp7 escherichia
147	82	6.9	472	2	070J50_HAEIN	070j50 haemophilus	220	80.5	6.7	732	2	06S1Z5_ECOLI	06s1z5 escherichia
148	82	6.9	581	2	04R0M5_TETNG	04r0m5 tetraodon n	221	80.5	6.7	738	1	TRAD2_ECOLI	P22708 escherichia
149	82	6.9	587	2	06C0H8_YARLI	06c0h8 yarrowia li	222	80.5	6.7	738	2	07AK62_9ZZZB	07ak62 plasmodi r10
150	82	6.9	589	1	RGPI_MOUSE	P46061 mus musculu	223	80.5	6.7	891	1	VP4A_VACCC	P20642 vaccinia vi
151	82	6.9	589	2	091Y52_MOUSE	091y52 mus musculu	224	80.5	6.7	891	1	VP4A_VACCV	P16715 vaccinia vi
152	82	6.9	589	2	08C2E3_MOUSE	08c2e3 mus musculu	225	80.5	6.7	891	2	051XQ4_MONPV	051xq4 monkeypox v
153	82	6.9	589	2	06NZB5_MOUSE	06nzb5 mus musculu	226	80.5	6.7	891	2	076ZQ5_PPOXY	076zq5 vaccinia vi
154	82	6.9	646	2	06ZPH4_MOUSE	06zph4 mus musculu	227	80.5	6.7	891	2	08V4W5_MONPV	08v4w5 monkeypox v
155	82	6.9	647	2	08PXU3_METMA	08pxu3 methanogarc	228	80.5	6.7	1687	2	07SC49_NEUCR	07sc49 neuropept
156	82	6.9	647	2	04HUJ3_CAMLA	04huj3 campylobact	229	80.5	6.7	1780	2	09ZTR82_ARATH	09ztr82 arabidopsis
157	82	6.9	819	2	04UCD0_SULAC	Q4jcd0 sulfolobus	230	80	6.7	103	2	09RXJ3_DEIRA	09rxj3 deinococcus
158	82	6.9	989	2	06CDB6_YARLI	06cdb6 yarrowia li	231	80	6.7	156	2	081513_9HEPC	081513 heparitis c
159	82	6.9	1031	2	081564_PLAF7	P81564 plasmodium	232	80	6.7	197	2	07YWX2_CABEL	07ywx2 caenorhabdi
160	82	6.9	1466	2	P78576_EMENT	P78576 escherichia	233	80	6.7	238	2	05QTD8_HUMAN	05qtd8 homo sapien
161	82	6.9	1466	2	05AS02_EMENT	05as02 aspergillus	234	80	6.7	238	2	09SKH1_MACPA	09skh1 macaca fasc
162	81.5	6.8	190	2	09KIT9_ECOLI	Q9kit9 escherichia	235	80	6.7	255	2	06V7H6_EAV	06v7h6 equine arte
163	81.5	6.8	283	2	05IDJ3_ENTHI	Q5idj3 entamoeba n	236	80	6.7	280	2	04MTK3_BACCE	04mtk3 bacillus ce
164	81.5	6.8	297	2	09B893_YTREM	09b893 schistosoma	237	80	6.7	280	2	0635R8_BAC CZ	0635r8 bacillus ce
165	81.5	6.8	311	2	08CD14_MOUSE	Q8cd14 mus musculu	238	80	6.7	280	2	06HEF5_BAC CZ	06hef5 bacillus th
166	81.5	6.8	349	1	RNFD_PASMU	Q9cmj3 passerella	239	80	6.7	280	2	0731V3_BACCI	0731v3 bacillus ce
167	81.5	6.8	352	2	09HTF5_HUMAN	Q9htf5 homo sapien	240	80	6.7	280	2	0819H0_BACCR	0819h0 bacillus ce
168	81.5	6.8	387	2	072C77_PBSVA	Q72c77 desulfovibr	241	80	6.7	280	2	081MWO_BACAN	081mwo bacillus an
169	81.5	6.8	391	2	04VBD2_MOUSE	Q4vbd2 mus musculu	242	80	6.7	280	2	07A5V6_STAN	07a5v6 bacillus lococ
170	81.5	6.8	414	2	06PAH4_MOUSE	Q6pah4 mus musculu	243	80	6.7	290	2	099UM2_STAM	099um2 staphylococ
171	81.5	6.8	438	2	08CSB1_MOUSE	Q8csb1 mus musculu	244	80	6.7	300	2	09C840_ARATH	09c840 arabidopsis
172	81.5	6.8	438	2	035934_MOUSE	Q35934 mus musculu	245	80	6.7	309	1	RTM1_YEAST	P40113 saccharomyc
173	81.5	6.8	465	2	07VRC0_CANRP	Q7vrc0 candidatus	246	80	6.7	343	2	07UBS9_RHOBA	07ubs9 rhodospirell
174	81.5	6.8	465	2	0803C9_BRARE	Q803c9 brachydanio	247	80	6.7	347	2	09PFM1_ARATH	09pfm1 arabidopsis
175	81.5	6.8	519	2	09NVS8_HUMAN	Q9nv88 homo sapien	248	80	6.7	355	2	073J45_TREDE	073j45 treponema d
176	81.5	6.8	577	2	06P126_HUMAN	Q6p126 homo sapien	249	80	6.7	359	2	07NAF8_PHOTO	07naf8 photorhabdu
177	81.5	6.8	577	2	072748_HUMAN	Q72748 homo sapien	250	80	6.7	360	2	09H1X3_HUMAN	09h1x3 homo sapien



251	80	6.7	388	2	058427_PYRO	058427_Pyrococcus	324	78.5	6.6	538	2	04HP8_CAMCO	04HP8_campylobact
252	80	6.7	488	2	0650S8_ORISA	0650S8_Oryza sativ	325	78.5	6.6	557	2	05CXU4_CRYFV	05CXU4_cryptospori
253	80	6.7	540	2	06FX17_CANGA	06FX17_candida gla	326	78.5	6.6	666	1	KUP_STFAS	08d21_mus muscucu
254	80	6.7	554	2	04PC93_USTWA	04PC93_ustiliago ma	327	78.5	6.6	678	2	061710_MOUSE	061710_mus muscucu
255	80	6.7	650	2	0699F8_AMOCA	0699F8_anopheles g	328	78.5	6.6	681	2	0769F3_HUMAN	0769F3_homo sapien
256	80	6.7	661	2	0759Y6_ASHGO	0759Y6_ashya goss	329	78.5	6.6	683	2	0769F4_HUMAN	0769F4_homo sapien
257	80	6.7	680	2	07VH08_HEHLP	07VH08_helicobacte	330	78.5	6.6	726	2	04UC59_THEAN	04UC59_theliera a
258	80	6.7	700	2	072021_LISMF	072021_listeria mo	331	78.5	6.6	766	1	ABCP9_HUMAN	09p78_homo sapien
259	80	6.7	893	2	0417J8_GIBZE	0417J8_gibberella	332	78.5	6.6	769	2	06P2Q0_HUMAN	06P2Q0_homo sapien
260	80	6.7	3010	2	0901Y9_9HEPC	0901Y9_hepatitis c	333	78.5	6.6	796	2	05W9G7_HUMAN	05W9G7_homo sapien
261	79.5	6.7	266	2	051PE9_9RODE	051PE9_pernonachus	334	78.5	6.6	867	2	04N908_THEPA	04N908_theliera p
262	79.5	6.7	266	2	051PE9_9RODE	051PE9_pernonachus	335	78.5	6.6	1308	2	04XVA2_PLACH	04XVA2_plasmodium
263	79.5	6.7	269	2	0722B0_LISMF	0722B0_listeria mo	336	78.5	6.6	6473	2	081KM9_PLAF7	081KM9_plasmodium
264	79.5	6.7	307	2	089NC2_BRAVA	089NC2_bradryrhizod	337	78	6.5	188	2	081YM2_BACON	081YM2_bacillus an
265	79.5	6.7	367	2	08ESY3_OCEIH	08ESY3_oceanobacil	338	78	6.5	219	2	08W2Y0_ORISA	08W2Y0_oryza sativ
266	79.5	6.7	379	2	0508J9_9RODE	0508J9_pernonachus	339	78	6.5	226	2	09CPF6_PASNU	09CPF6_pasteurella
267	79.5	6.7	391	2	06TY96_9BILA	06TY96_xiphinema a	340	78	6.5	240	2	09CPF6_PASNU	09CPF6_pasteurella
268	79.5	6.7	438	1	CLN3_CAMPA	029611_cantis famli	341	78	6.5	245	2	P94625_CLODI	094625_clostridium
269	79.5	6.7	463	2	092EL3_LISIN	092EL3_listeria in	342	78	6.5	252	2	06B8K2_GRATL	06B8K2_gracillaria
270	79.5	6.7	488	2	06QU70_ASPMG	06QU70_aspergillus	343	78	6.5	329	2	09KD13_BACHD	09KD13_bacillus ha
271	79.5	6.7	491	1	VIE1_HCMVT	P03169_human cytom	344	78	6.5	331	2	09KXC4_SUTRO	09KXC4_sulfolobus
272	79.5	6.7	546	1	FLVC2_RAT	P00815_rattus norv	345	78	6.5	339	2	08D4K9_VIBVU	08D4K9_vibrio vuln
273	79.5	6.7	549	2	04Z2E3_PLABE	04Z2E3_plasmodium	346	78	6.5	357	2	095IA3_TERTH	095IA3_tetrahymena
274	79.5	6.7	598	2	051954_BORHE	051954_borrelia the	347	78	6.5	360	2	097HC3_CLOAB	097HC3_clostridium
275	79.5	6.7	649	2	08BZ08_DEBHA	08BZ08_debrayomyce	348	78	6.5	382	2	08TW61_METAC	08TW61_methanosarc
276	79.5	6.7	674	2	086P19_DROME	086P19_drosophila	349	78	6.5	414	2	08D5Y9_VIBVU	08D5Y9_vibrio vuln
277	79.5	6.7	726	2	09EUJ3_SALET	09EUJ3_salmonella	350	78	6.5	428	2	09JRS0_ACTAC	09JRS0_actinobacil
278	79.5	6.7	732	2	05J497_SALCH	05J497_salmonella	351	78	6.5	442	2	07MD08_VIBVU	07MD08_vibrio vuln
279	79.5	6.7	748	2	04WB47_ASPFU	04WB47_aspergillus	352	78	6.5	471	1	Y872_HAEIN	06HMA8_BACHK
280	79.5	6.7	784	2	09VYV0_DROME	09VYV0_drosophila	353	78	6.5	486	2	06HMA8_BACHK	06HMA8_bacillus th
281	79.5	6.7	784	2	08KDB0_CHUTE	08KDB0_chlorobium	354	78	6.5	545	2	06FPM9_CANGA	06FPM9_candida gla
282	79.5	6.7	818	2	05HXC6_CAMUR	05HXC6_campylobact	355	78	6.5	555	2	06FPM9_CANGA	06FPM9_candida gla
283	79.5	6.7	1708	2	04LE27_HUMAN	04LE27_homo sapien	356	78	6.5	641	2	09LIC2_ARATH	09LIC2_arabidopsis
284	79.5	6.7	3409	2	07S127_NEUCR	07S127_neurospora	357	78	6.5	658	2	07QG08_ANODA	07QG08_actinobacil
285	79.5	6.6	114	2	06VR66_HELPY	06VR66_helicobacte	358	78	6.5	1297	2	09Y817_SCHPO	09Y817_haemophilus
286	79	6.6	251	2	06M012_METUP	06M012_methanococ	359	78	6.5	1297	2	09Y817_SCHPO	09Y817_haemophilus
287	79	6.6	300	2	080ZH3_5MURI	080ZH3_arvicanthis	360	78	6.5	2136	1	YCF2_MARPO	YCF2_marchantia
288	79	6.6	308	2	08RGW6_FUSUN	08RGW6_fusobacteri	361	78	6.5	7180	1	RIAB_CVMJH	RIAB_cymjha
289	79	6.6	312	2	06KH29_MYCNO	06KH29_mycoplasma	362	77.5	6.5	116	2	0976T7_SUTRO	0976T7_sulfolobus
290	79	6.6	290	2	07KS19_DROME	07KS19_drosophila	363	77.5	6.5	190	2	09K1AB_ECOLI	09K1AB_escherichia
291	79	6.6	349	1	RMFD_BTUCAP	08KA19_buchnera ap	364	77.5	6.5	263	2	04MOY0_BACCE	04MOY0_bacillus ce
292	79	6.6	356	2	05X8T4_LEGPA	05X8T4_legionella	365	77.5	6.5	263	2	073DX2_BACCI	073DX2_bacillus ce
293	79	6.6	356	2	07MG43_VIBVU	07MG43_vibrio vuln	366	77.5	6.5	263	2	081I83_BACCR	081I83_bacillus ce
294	79	6.6	375	2	04ZXH6_PSEST	04ZXH6_pseudomonas	367	77.5	6.5	266	2	051PE6_PERO	051PE6_pernonachus
295	79	6.6	375	2	0887L9_PSESM	0887L9_pseudomonas	368	77.5	6.5	269	2	08Y8T5_LISMO	08Y8T5_listeria mo
296	79	6.6	443	2	0523L2_MAGGR	0523L2_magnaporthe	369	77.5	6.5	270	2	08H1Y4_PERO	08H1Y4_pernonachus
297	79	6.6	484	2	06NIB0_CORDI	06NIB0_corynebacte	370	77.5	6.5	270	2	08H1Y2_PERO	08H1Y2_pernonachus
298	79	6.6	754	2	051PY0_MAGGR	051PY0_magnaporthe	371	77.5	6.5	270	2	08H1Y2_PERO	08H1Y2_pernonachus
299	79	6.6	770	2	05LA24_BACRN	05LA24_bacteroides	372	77.5	6.5	294	2	08E3L0_OCEFH	08E3L0_oceanobacil
300	79	6.6	828	2	064QD3_BACFR	064QD3_bacteroides	373	77.5	6.5	299	2	08ZAL1_YERPE	08ZAL1_yersinia pe
301	79	6.6	1531	2	04RGAB_TETNG	04RGAB_tetradodon n	374	77.5	6.5	299	2	066FT9_YERPS	066FT9_yersinia ps
302	79	6.6	1679	2	096L95_HUMAN	096L95_homo sapien	375	77.5	6.5	310	2	08D1I6_YERPE	08D1I6_yersinia pe
303	79	6.6	1780	2	061TR7_HUMAN	061TR7_homo sapien	376	77.5	6.5	327	2	09POG1_YERPA	09POG1_yersinia pe
304	79	6.6	2751	2	04Y3S8_PLACH	04Y3S8_plasmodium	377	77.5	6.5	328	2	09K6M6_BACHD	09K6M6_bacillus ha
305	79	6.6	3010	2	09J3H8_9HEPC	09J3H8_hepatitis c	378	77.5	6.5	338	2	042882_SCHRO	042882_schistosach
306	79	6.6	3010	2	09Q1Z0_9HEPC	09Q1Z0_hepatitis c	379	77.5	6.5	355	2	08R770_THETN	08R770_thermoaer
307	79	6.6	3010	2	Y350_MYCCPN	P75428_mycoplasma	380	77.5	6.5	355	2	04R2P6_VARIH	04R2P6_vargula hii
308	78.5	6.6	263	2	04Z3F6_PLABE	04Z3F6_plasmodium	381	77.5	6.5	377	2	04R2P6_VARIH	04R2P6_vargula hii
309	78.5	6.6	266	2	051PE7_9RODE	051PE7_pernonachus	382	77.5	6.5	377	2	04R2P6_VARIH	04R2P6_vargula hii
310	78.5	6.6	269	2	092D15_LISIN	092D15_listeria in	383	77.5	6.5	377	2	04R2P6_VARIH	04R2P6_vargula hii
311	78.5	6.6	292	2	05V6V4_HALMA	05V6V4_haloaerula	384	77.5	6.5	377	2	04R2P6_VARIH	04R2P6_vargula hii
312	78.5	6.6	313	2	0910B3_STRCC	0910B3_streptomyce	385	77.5	6.5	377	2	04R2P6_VARIH	04R2P6_vargula hii
313	78.5	6.6	353	2	04L0T2_CAMLA	04L0T2_campylobact	386	77.5	6.5	377	2	04R2P6_VARIH	04R2P6_vargula hii
314	78.5	6.6	358	1	RMFD_HAEIN	051288_haemophilus	387	77.5	6.5	392	2	08G7P7_BIFLO	08G7P7_biflobosach
315	78.5	6.6	358	1	RMFD_HAEIN	051288_haemophilus	388	77.5	6.5	392	2	09P6M5_SCHPO	09P6M5_schistosach
316	78.5	6.6	380	2	06QJ05_HAE18	06QJ05_haemophilus	389	77.5	6.5	411	2	09P6M5_SCHPO	09P6M5_schistosach
317	78.5	6.6	380	2	06A8F8_BACTN	06A8F8_bacteroides	390	77.5	6.5	422	2	09HXC6_THRAC	09HXC6_thermoplas
318	78.5	6.6	382	2	05LE17_BACFN	05LE17_bacteroides	391	77.5	6.5	422	2	09HXC6_THRAC	09HXC6_thermoplas
319	78.5	6.6	382	2	064V54_BACFR	064V54_bacteroides	392	77.5	6.5	430	2	05MUU7_LEGFL	05MUU7_legionella
320	78.5	6.6	418	2	065LP8_BACLD	065LP8_bacillus 11	393	77.5	6.5	440	2	09Z1Z3_PEDMN	09Z1Z3_peditomonas
321	78.5	6.6	451	2	065UD5_MANSM	065UD5_mannheimia	394	77.5	6.5	458	2	062X71_BACLD	062X71_bacillus 11
322	78.5	6.6	471	1	5HT2A_CRIGR	P18599_cricetella su	395	77.5	6.5	481	2	04P6B0_USTWA	04P6B0_ustiliago ma
323	78.5	6.6	512	2	08G1D7_BRUSU	08G1D7_brucella su	396	77.5	6.5	483	2	09G8V8_9CRYP	09G8V8_rhodomonas

397	77.5	6.5	491	2	028284_ARCFU	028284_archaeoglob	470	77	6.4	3010	2	081757_9HBP	081757_hepatitis c
398	77.5	6.5	491	2	06SX0_HCMV	06sx0 human cytom	471	77	6.4	3010	2	09J3G4_9HEPC	09j3g4 hepatitis c
399	77.5	6.5	491	2	057DX0_BRUNB	057dx0 bruceella ab	472	77	6.4	3013	2	06J6P5_9HEPC	06j6p5 hepatitis c
400	77.5	6.5	532	2	08YGI2_BRUNE	08ygi2 bruceella me	473	77	6.4	4416	2	09J3F3_9CORO	09j3f3 murine hepa
401	77.5	6.5	538	2	04HP2_CAMUP	04hp2 campylobact	474	77	6.4	4416	2	09J3F8_9CORO	09j3f8 murine hepa
402	77.5	6.5	556	2	089180_VAV	089180 variola vir	475	77	6.4	7124	1	RIAB_CW2	09p3f3 m replicase
403	77.5	6.5	556	2	089232_VAV	089232 variola vir	476	76.5	6.4	253	3	051PE6_PERLO	051pe6 perognathus
404	77.5	6.5	567	2	07RNKO_PLAYO	07rnko plasmodium	477	76.5	6.4	266	2	051PE8_PERLO	051pe8 perognathus
405	77.5	6.5	572	2	04XZG8_PLACH	04xzg8 plasmodium	478	76.5	6.4	278	2	08XBF0_ECO57	08xf0 escherichia
406	77.5	6.5	618	2	059P22_CANAL	059p22 candida alb	479	76.5	6.4	281	2	08XBF9_9BILA	08xf9 ancylostoma
407	77.5	6.5	620	2	08ERX1_SHEON	08erx1 shewanella	480	76.5	6.4	282	2	092WV5_RHIME	092wv5 thryobulum m
408	77.5	6.5	676	2	04RUC9_TETNG	04ruc9 tetraodon n	481	76.5	6.4	342	2	072290_CABEL	072290 caenorhabd1
409	77.5	6.5	734	1	NU5C_ORYSA	P12129 oryza sativ	482	76.5	6.4	352	1	RNPD_SALT1	082668 salmonella
410	77.5	6.5	788	2	04K519_PSEFS	04k519 pseudomonas	483	76.5	6.4	352	1	RNPD_SALT1	082668 salmonella
411	77.5	6.5	892	1	VP4A_VAV	P33817 variola vir	484	76.5	6.4	352	2	05PTI1_SALCH	05pti1 salmonella
412	77.5	6.5	892	2	09ONT0_VAV	09ont0 variola min	485	76.5	6.4	352	2	05PTC8_SALPA	05ptc8 salmonella
413	77.5	6.5	979	2	07MLV5_VIBV	07mlv5 vibrio vuln	486	76.5	6.4	379	1	CYB_DIFOR	09ga3 dipodomys o
414	77.5	6.5	1033	2	05BL65_XENTR	05bl65 xenopus tro	487	76.5	6.4	379	2	09GBY7_OCCHA	09gb7 ochotona pa
415	77.5	6.5	1140	2	05CTR7_CRYPV	05ctr7 cryptospori	488	76.5	6.4	379	2	0508L8_9RODE	0508l8 dipodomys m
416	77.5	6.5	1476	2	08T66_DICDI	08t66 dictyostel	489	76.5	6.4	379	2	0508J5_PERLO	0508j5 perognathus
417	77.5	6.5	1794	2	025377_LOLOP	025377 loligo opal	490	76.5	6.4	379	2	0508J3_9RODE	0508j3 perognathus
418	77.5	6.5	1959	2	05ZSB8_ORYSA	05zsb8 oryza sativ	491	76.5	6.4	380	2	08HNT7_PRAHA	08hnt7 praomys nat
419	77.5	6.5	2141	2	0869H2_LYMS	0869h2 lymaea sta	492	76.5	6.4	391	2	04S1Z9_TETNG	04s1z9 tetraodon n
420	77.5	6.5	6680	2	05CX17_CRYPV	05cx17 cryptospori	493	76.5	6.4	435	2	08KHK2_PSEAE	08khk2 pseudomonas
421	77	6.4	170	2	072UC4_LEPIC	072uc4 leptospira	494	76.5	6.4	435	2	05UBS7_ECOLI	05ubs7 escherichia
422	77	6.4	170	2	08FOO4_LEPIN	08foo4 leptospira	495	76.5	6.4	435	2	07UBJ3_SHIFL	07ubj3 shigella fl
423	77	6.4	255	2	09BVN5_RAV	09bvns equine arte	496	76.5	6.4	435	2	083PL5_SHIFL	083pl5 shigella fl
424	77	6.4	286	2	061082_BACAN	061082 bacillus an	497	76.5	6.4	438	1	CLN3_MOUSE	061124 mus musculu
425	77	6.4	286	2	073A28_BACCI	073a28 bacillus ce	498	76.5	6.4	439	2	05LEQ8_BACRN	05leq8 bacteroides
426	77	6.4	287	2	0541L2_DICDI	0541l2 dictyostel	499	76.5	6.4	439	2	064SN0_BACRN	064sn0 bacteroides
427	77	6.4	315	2	04HEF7_CAMCO	04hef7 campylobact	500	76.5	6.4	451	2	0660T8_BORCA	0660t8 borrelia ga
428	77	6.4	332	2	09XTM3_CAEEL	09xtm3 caenorhabd1	501	76.5	6.4	453	2	06ZGZ4_ORYSA	06zgz4 oryza sativ
429	77	6.4	353	1	MTRIA_MOUSE	061184 mus musculu	502	76.5	6.4	462	2	082V00_NITFU	082v00 nitrosomona
430	77	6.4	379	2	08WEK6_THORA	08wek6 thomomys ta	503	76.5	6.4	468	1	YDBM_CABEL	019084 caenorhabd1
431	77	6.4	383	2	08TZC2_METKA	08tzc2 methanomyru	504	76.5	6.4	480	2	06SKJ9_HCMV	06skj9 human cytom
432	77	6.4	386	2	07MX00_PORGI	07mx00 porphyromon	505	76.5	6.4	491	2	06SWP6_HCMV	06swp6 human cytom
433	77	6.4	419	2	P94949_METKA	P94949 methanomyru	506	76.5	6.4	500	2	096ZM3_SULTO	096zm3 sulfolobus
434	77	6.4	423	2	071X88_LISMF	071x88 listeria mo	507	76.5	6.4	526	1	FLVC2_HUMAN	053z3 homo sapien
435	77	6.4	430	2	08U1Z6_PYRPU	08u1z6 pyrococcus	508	76.5	6.4	526	2	053ZT9_HUMAN	053zt9 homo sapien
436	77	6.4	435	2	073RD9_TREDE	073rd9 treponema d	509	76.5	6.4	528	2	07VP70_HABED	07vp70 haemophilus
437	77	6.4	444	2	06GD70_STAAS	06gd70 staphylococ	510	76.5	6.4	538	2	05HWZ4_CAMJR	05hwz4 campylobact
438	77	6.4	444	2	08NYX5_STAAS	08nyx5 staphylococ	511	76.5	6.4	538	2	09PTV5_CAMCE	09ptv5 campylobact
439	77	6.4	481	2	04QWV3_ASFPU	04qwv3 aspergillus	512	76.5	6.4	555	2	08NBG4_HUMAN	08nbg4 homo sapien
440	77	6.4	490	2	014670_HUMAN	014670 homo sapien	513	76.5	6.4	560	2	0627P1_CAEER	0627p1 caenorhabd1
441	77	6.4	491	2	09T251_PHYTN	09t251 phytophhor	514	76.5	6.4	570	2	07Z6J6_HUMAN	07z6j6 homo sapien
442	77	6.4	505	2	04UT66_TREAN	04ut66 thelletaria a	515	76.5	6.4	589	2	09ZLJ1_HELPJ	09zl1 helicobacte
443	77	6.4	519	2	09ASQ7_ARATH	09asq7 arabidopsis a	516	76.5	6.4	614	2	057TU9_BRUNB	057tu9 bruceella ab
444	77	6.4	537	2	0518N5_ENTHI	0518n5 entamoeba h	517	76.5	6.4	614	2	08FWB2_BRUSU	08fwb2 bruceella su
445	77	6.4	559	2	09AAX4_CAUCH	09aax4 caulobacter	518	76.5	6.4	615	2	05JF60_PYRKO	05jf60 pyrococcus
446	77	6.4	590	1	NU5M_TRYBB	P84540 trypanosoma	519	76.5	6.4	619	2	074520_SCHPO	074520 schizosacch
447	77	6.4	606	2	04NSD5_9DELT	04nsd5 anaeromyxob	520	76.5	6.4	687	2	074520_SCHPO	074520 schizosacch
448	77	6.4	616	2	05WZK7_SULTS	05wz27 sulfolobus	521	76.5	6.4	743	2	08XNB0_CLOPE	08xnb0 clostridium
449	77	6.4	650	2	06G6J3_STAAS	06g6j3 staphylococ	522	76.5	6.4	775	2	04NKA4_THEPA	04nka4 thelletaria p
450	77	6.4	650	2	06GDI1_STAAR	06gdi1 staphylococ	523	76.5	6.4	839	2	0918C9_CHICK	0918c9 gallus gall
451	77	6.4	650	2	05HCO6_STAAC	05hco6 staphylococ	524	76.5	6.4	902	2	041IV8_GIBZE	041iv8 gibberella
452	77	6.4	650	2	07A374_STAAN	07a374 staphylococ	525	76.5	6.4	909	2	054BU4_DICDI	054bu4 dictyostel
453	77	6.4	650	2	08NUK4_STAAM	08nuk4 staphylococ	526	76.5	6.4	909	2	08T9M6_DICDI	08t9m6 dictyostel
454	77	6.4	650	2	099QZ7_STAMV	099qz7 staphylococ	527	76.5	6.4	1485	2	08EUA2_MYCPE	08eua2 mycoplasma
455	77	6.4	722	2	063ZK1_BACCE	063zk1 bacillus ce	528	76.5	6.4	1641	2	06BSZ7_DEBNA	06bsz7 debaryomyce
456	77	6.4	738	1	FTSK_STAM	081838 arabidopsis	529	76	6.4	156	2	0815O4_9HEPC	0815o4 hepatitis c
457	77	6.4	789	1	06Z9F7_STAAS	06z9f7 staphylococ	530	76	6.4	201	2	06MT09_MYCMS	06mt09 mycoplasma
458	77	6.4	836	2	07Z1F2_PLAFA	07z1f2 plasmodium	531	76	6.4	210	2	08PYL0_METWA	08pyl0 methanosaac
459	77	6.4	836	2	07Z1F2_PLAFA	07z1f2 plasmodium	532	76	6.4	255	2	06V715_EAV	06v715 equine arte
460	77	6.4	877	2	0750H8_ASHCO	0750h8 ashbya goss	533	75	6.4	272	2	08R7J2_THERN	08r7j2 thermoaaner
461	77	6.4	991	2	0813J0_ARATH	0813j0 arabidopsis	534	76	6.4	282	2	08EUD4_OCEAN	08eud4 oceanobacil
462	77	6.4	1024	2	07Z1F1_PLAFA	07z1f1 plasmodium	535	76	6.4	325	2	09Z2H9_MESAV	09z2h9 mesocricetu
463	77	6.4	1024	2	081XZ6_PLAF7	081x6 plasmodium	536	76	6.4	342	1	NU2M_LOCOM	036426 locusta mig
464	77	6.4	1025	2	025693_PLAFA	025693 plasmodium	537	76	6.4	346	2	04H7X1_9DEIO	04h7x1 diinococcus
465	77	6.4	1117	2	09M133_ARATH	09m133 arabidopsis	538	75	6.4	402	2	0219J3_CABEL	0219j3 caenorhabd1
466	77	6.4	1477	2	06FTF9_CANGA	06ftf9 candida gla	539	76	6.4	425	2	09JRS2_ACTAC	09jrs2 actinobacil
467	77	6.4	1500	2	09ZU84_ARATH	09zu84 arabidopsis	540	76	6.4	438	2	08BHG7_PSEBK	08bhg7 pseudomonas
468	77	6.4	1814	2	06OWH4_CAEER	06owh4 caenorhabd1	541	76	6.4	461	2	085U02_STRPN	085u02 streptococc
469	77	6.4	3010	2	068788_9HEPC	068788 hepatitis c	542	76	6.4	474	2	08F2K0_LEPIN	08f2k0 leptospira

543	76	6.4	474	2	Q72SX4_LEPITC	Q72sx4 leptopipta	616	75.5	6.3	491	2	Q6SW2_HCMV	Q6sw2 human cytom
544	76	6.4	519	2	Q852P3_PERRR	Q852p3 perilla fru	617	75.5	6.3	491	2	Q6SWY1_HCMV	Q6swy1 human cytom
545	76	6.4	567	2	Q6NXT6_HUMAN	Q6nxt6 homo sapien	618	75.5	6.3	498	2	Q475J3_CHIEU	Q475j3 chlamydom
546	76	6.4	616	2	Q7OMX6_GIALA	Q7omx6 giardia lam	619	75.5	6.3	501	2	Q6CH25_YARLI	Q6chs2 yarrowia 11
547	76	6.4	669	2	Q9L2Z7_ARATY	Q9l2z7 arabisdopsis	620	75.5	6.3	539	2	Q5CIS2_CRYHO	Q5cis2 cryospori
548	76	6.4	699	2	Q6IVM6_GANAM	Q6ivm6 uncultured	621	75.5	6.3	551	1	FLVCC2_MOUSE	Q9lxm5 mus musculu
549	76	6.4	851	2	Q6CKR4_KLUUA	Q6ckr4 kluyveromyc	622	75.5	6.3	593	2	Q253J2_HELIPY	Q253j2 helicobacte
550	76	6.4	931	2	Q6CKR4_KLUUA	Q6ckr4 kluyveromyc	623	75.5	6.3	646	2	Q5ZIM5_CHICK	Q5zlm5 gallus gall
551	76	6.4	953	2	Q7BNO_MYCGA	Q7bno mycoplasma	624	75.5	6.3	708	2	Q22806_CAEEL	Q22806 caenorhabdi
552	76	6.4	1041	2	Q5Z570_ORYSA	Q5z570 oryza sativ	625	75.5	6.3	746	2	Q8PGM4_XANAC	Q8pgm4 xanthomonas
553	76	6.4	1306	1	Q7PVU9_ANOGA	Q7pvu9 anopheles g	626	75.5	6.3	773	2	Q963J25_ARATH	Q963j25 arabidopsis
554	76	6.4	1450	1	Q6TX9_CAEEL	Q6tx9 caenorhabdi	627	75.5	6.3	795	1	CLCA_ARATH	P92941 arabidopsis
555	76	6.4	1481	2	Q9T79_RABIT	Q9t79 cyccolagus	628	75.5	6.3	795	2	Q6LIT6_CABER	P92941 arabidopsis
556	76	6.4	1551	2	Q96WN4_VENIN	Q96wn4 venturia in	629	75.5	6.3	858	2	Q52B43_MAGGR	Q52b43 magnaporthe
557	76	6.4	1873	2	Q18698_CAEEL	Q18698 caenorhabdi	630	75.5	6.3	939	2	Q5B634_EMENI	Q5b634 aspergillus
558	76	6.4	1877	2	Q8MQA1_CAEEL	Q8mqal caenorhabdi	631	75.5	6.3	1008	2	Q89154_9HEPC	Q89154 hepatictis c
559	76	6.4	2009	2	Q7RBP2_PLAYO	Q7rbp2 plasmodium	632	75.5	6.3	1088	2	Q4UI92_THEAN	Q4ui92 theileria a
560	76	6.4	3010	2	P90191_9HEPC	P90191 plasmodium	633	75.5	6.3	1142	2	Q9UT41_SCHRO	Q9ut41 schistosach
561	76	6.4	3010	2	P90193_9HEPC	P90193 hepatictis c	634	75.5	6.3	1583	2	Q7P6S4_RICSI	Q7p6s4 rickettsia
562	76	6.4	3010	2	P90194_9HEPC	P90194 hepatictis c	635	75.5	6.3	3010	2	Q9J3G7_9HEPC	Q9j3g7 hepatictis c
563	75.5	6.3	156	1	MTR1A_RAT	P49218 rattus norv	636	75	6.3	105	2	Q5AM04_CANAL	Q5am04 candida alb
564	75.5	6.3	162	2	Q6PG7_XENLA	Q6pgp7 xenopus lae	637	75	6.3	132	2	Q6N505_RHOPA	Q6n505 rhodopseudo
565	75.5	6.3	206	2	Q61TR8_CABER	Q61tr8 caenorhabdi	638	75	6.3	152	2	Q4TPK6_9SPHN	Q4tpk6 erythroba
566	75.5	6.3	220	2	Q633A3_BACCZ	Q633a3 bacillus ce	639	75	6.3	156	2	Q81498_9HEPC	Q81498 hepatictis c
567	75.5	6.3	228	2	Q9VUN8_DROME	Q9vun8 drosophila	640	75	6.3	166	2	Q81507_9HEPC	Q81507 hepatictis c
568	75.5	6.3	231	2	Q6MD11_PARUM	Q6md11 paracitlamyd	641	75	6.3	166	2	Q81531_9HEPC	Q81531 hepatictis c
569	75.5	6.3	244	2	Q6B927_GRATL	Q6b927 gratiaria	642	75	6.3	170	2	Q4Y7N2_PLACH	Q4y7n2 plasmodium
570	75.5	6.3	247	2	Q7P13_RAT	Q7p13 rattus norv	643	75	6.3	215	2	Q34238_CAPSU	Q34238 capricornis
571	75.5	6.3	248	2	Q6HMF5_BACHK	Q6hmf5 bacillus th	644	75	6.3	218	2	Q6SKB1_ARTAU	Q6skb1 arthrobacte
572	75.5	6.3	263	2	Q63E29_BACCZ	Q63e29 bacillus ce	645	75	6.3	220	2	Q5FPJ3_BHRGG	Q5fpj3 ethiopia x
573	75.5	6.3	263	2	Q6HNS6_BACHK	Q6hns6 bacillus th	646	75	6.3	220	2	Q419S9_STAHJ	Q419s9 streptococ
574	75.5	6.3	263	2	Q8CYF4_STRPN	Q8cyf4 streptococc	647	75	6.3	225	2	Q6VMD0_SCORO	Q6vmd0 scoro
575	75.5	6.3	263	2	Q97PD2_STRPN	Q97pd2 streptococc	648	75	6.3	227	2	Q9GAT3_OCHHT	Q9gat3 ochotona hy
576	75.5	6.3	263	2	Q63GB2_BACCZ	Q63gb2 bacillus ce	649	75	6.3	228	2	Q4YQ66_PLABE	Q4yq66 plasmodium
577	75.5	6.3	263	2	Q81YU8_BACAN	Q81yu8 bacillus an	650	75	6.3	249	1	Y1368_METUA	Y1368 metua
578	75.5	6.3	266	2	Q51PF7_GRODE	Q51pf7 perognathus	651	75	6.3	256	2	Q631U3_BACCZ	Q631u3 bacillus ce
579	75.5	6.3	269	2	Q66PG6_XENLA	Q66pg6 xenopus lae	652	75	6.3	274	2	Q9KND0_VIBCH	Q9knd0 vibrio chol
580	75.5	6.3	278	2	Q66SK7_MACEU	Q66sk7 macropus eu	653	75	6.3	277	2	Q6NNA3_DBERA	Q6nna3 bdellovibri
581	75.5	6.3	301	2	Q5C281_SCHJA	Q5c281 schistosoma	654	75	6.3	294	2	Q8RET4_FUSNN	Q8ret4 fusobacteri
582	75.5	6.3	303	2	Q9KZ08_STRCO	Q9kz08 streptomyce	655	75	6.3	302	2	Q6CVR2_KLUUA	Q6cvr2 kluyveromyc
583	75.5	6.3	305	2	Q4S7P1_TETNG	Q4s7p1 tetradodon n	656	75	6.3	311	2	Q5ZL68_CHICK	Q5ztl68 gallus gall
584	75.5	6.3	310	2	Q870H5_YEAST	Q870h5 saccharomyc	657	75	6.3	318	2	Q4SMC3_TETNG	Q4smc3 tetradodon n
585	75.5	6.3	326	2	Q8ESU3_RAT	Q8esu3 rattus norv	658	75	6.3	330	2	Q58239_PYROCOC	Q58239 pyrococcus
586	75.5	6.3	339	2	Q9KSB3_VIBCH	Q9ksb3 vibrio chol	659	75	6.3	371	2	Q8BM45_MOUSE	Q8bm45 mus musculu
587	75.5	6.3	342	2	Q59TA5_CANAL	Q59tas candida alb	660	75	6.3	373	1	PE2R3_PIG	P5011 sus scrofa
588	75.5	6.3	352	1	Q9QEV3_HHV8	Q9qev3 human herpe	661	75	6.3	380	1	Q69GJ2_9PERO	Q69g2 rana rugosa
589	75.5	6.3	352	1	RNPD_ECO57	P58325 escherichia	662	75	6.3	380	2	Q46657_PIG	Q46657 sus scrofa
590	75.5	6.3	352	1	RNPD_ECOLI	P76184 escherichia	663	75	6.3	387	2	Q46657_PIG	Q46657 sus scrofa
591	75.5	6.3	352	1	Q8FPH4_ECOL6	P81h94 escherichia	664	75	6.3	407	2	Q7NRP5_CHRYO	Q7nrf5 chromobacte
592	75.5	6.3	352	2	Q83KY5_SHIFL	Q83ky5 shigella fl	665	75	6.3	418	2	Q6QPB8_LEGRN	Q6qpb8 legionella
593	75.5	6.3	377	2	Q4R2L1_VABRI	Q4r2l1 vargula h11	666	75	6.3	418	2	Q6ABT1_PROAC	Q6abt1 propionibac
594	75.5	6.3	379	1	CYB_ZAPFR	Q9xnm1 vargula h11	667	75	6.3	428	2	Q5WZ83_LEGPL	Q5wz83 legionella
595	75.5	6.3	379	2	Q508J8_PERPA	Q508j8 perognathus	668	75	6.3	428	2	Q5X7R2_LEGPA	Q5x7r2 legionella
596	75.5	6.3	389	2	Q8AY5_HYLA	Q8ay5 hyala japoni	669	75	6.3	424	2	Q4TP70_9SPHN	Q4tp70 erythroba
597	75.5	6.3	397	2	Q8AY5_HYLA	Q8ay5 caenorhabdi	670	75	6.3	425	2	Q4Z7S9_PLABE	Q4z7s9 plasmodium
598	75.5	6.3	397	2	Q8AY5_HYLA	Q8ay5 caenorhabdi	671	75	6.3	460	2	Q63QK3_BURPS	Q63qk3 burkholderi
599	75.5	6.3	400	2	Q421Y5_PLABE	Q421y5 plasmodium	672	75	6.3	460	2	Q6ZGF6_BURMA	Q6zgf6 burkholderi
600	75.5	6.3	410	2	Q70NM4_9BILA	Q70nm4 strongyloid	673	75	6.3	473	1	Q6BR1_HUMAN	Q6br1 homo sapien
601	75.5	6.3	413	2	Q5UET7_ECOLI	Q5uet7 escherichia	674	75	6.3	473	2	Q9BX06_HUMAN	Q9bx06 homo sapien
602	75.5	6.3	415	1	TNAB_ECO57	P21b13 escherichia	675	75	6.3	488	2	Q7RWS8_NEUCR	Q7rws8 neurospora
603	75.5	6.3	415	1	TNAB_ECOLI	P21b13 escherichia	676	75	6.3	498	2	Q75U67_FUGRU	Q75u67 fungu rubrif
604	75.5	6.3	415	1	Q5UEB4_ECOLI	Q5ueb4 escherichia	677	75	6.3	526	2	Q9SN21_ARATH	Q9sn21 arabidopsis
605	75.5	6.3	415	1	Q8FBN1_ECOL6	Q8fbn1 escherichia	678	75	6.3	543	2	Q7NS50_CHRYO	Q7ns50 chromobacte
606	75.5	6.3	415	1	Q8FBN1_ECOL6	Q8fbn1 escherichia	679	75	6.3	625	1	KUP2_LEBPH	Q5ztn5 legionella
607	75.5	6.3	433	2	Q6F3C9_CAEEL	Q6f3c9 caenorhabdi	680	75	6.3	649	2	Q34952_BACSV	Q34952 bacillus su
608	75.5	6.3	446	2	Q7S8U0_NEUCR	Q7s8u0 neurospora	681	75	6.3	662	2	Q7VED4_PROMA	Q7ved4 prochloroco
609	75.5	6.3	466	2	Q4Y729_PLACH	Q4y729 plasmodium	682	75	6.3	753	2	Q98S90_GUTTH	Q98s90 paramecium
610	75.5	6.3	471	1	SH72A_MOUSE	P33363 mus musculu	683	75	6.3	777	2	Q6BG55_PARRE	Q6bg55 gallinella
611	75.5	6.3	471	1	SH72A_MOUSE	P33363 mus musculu	684	75	6.3	838	2	Q4HZM9_GIBZE	Q4hzm9 gibberella
612	75.5	6.3	481	2	Q8COKO_MOUSE	Q8cok0 mus musculu	685	75	6.3	883	2	Q4N4L2_THEPA	Q4n4l2 theileria p
613	75.5	6.3	482	2	Q9P6J0_SCHPO	Q9p6j0 schistosach	686	75	6.3	885	2	Q8PU16_METPA	Q8pu16 methanoeac
614	75.5	6.3	491	2	Q6SWJ1_HCMV	Q6swj1 human cytom	687	75	6.3	937	2	Q82ZK7_ENTFA	Q82zk7 enterococcu
615	75.5	6.3	491	2	Q6SWM4_HCMV	Q6swm4 human cytom	688	75	6.3	1008	2	Q89153_9HEPC	Q89153 hepatictis c

689	75	6.3	1008	2	089156_9HEPC	089156 hepatitis c	762	74.5	6.2	377	2	Q4R1V3_VARH1	Q4R1V3 vargula h11
690	75	6.3	1008	2	089152_9HEPC	089152 hepatitis c	763	74.5	6.2	377	2	Q4R1V2_VARH1	Q4R1V2 vargula h11
691	75	6.3	1131	2	08NAT5_HUMAN	08nat5 homo sapien	764	74.5	6.2	377	2	Q4R2N2_VARH1	Q4R2N2 vargula h11
692	75	6.3	1135	2	08GUE7_GLITI	08gue7 cymodocea n	765	74.5	6.2	377	2	Q4R2N6_VARH1	Q4R2N6 vargula h11
693	75	6.3	1154	2	06FT16_CANCA	06ft16 candida gla	766	74.5	6.2	377	2	Q4R3E4_VARH1	Q4R3E4 vargula h11
694	75	6.3	1336	2	06F1J1_MESFL	06f1j1 mesoplasma	767	74.5	6.2	377	2	Q4R3G6_VARH1	Q4R3G6 vargula h11
695	75	6.3	1704	2	095206_9TRYP	095206 trypanosoma	768	74.5	6.2	377	2	Q4R3A9_VARH1	Q4R3A9 vargula h11
696	75	6.3	2248	1	CYAL_DROME	Cyalid4 drosophila	769	74.5	6.2	377	2	Q4R294_VARH1	Q4R294 vargula h11
697	75	6.3	2846	2	05SEL4_DICDI	05sel4 dicystois c	770	74.5	6.2	377	2	Q4R292_VARH1	Q4R292 vargula h11
698	75	6.3	3010	2	068833_9HEPC	068833 hepatitis c	771	74.5	6.2	377	2	Q4R2M9_VARH1	Q4R2M9 vargula h11
699	75	6.3	3010	2	09J3G2_9HEPC	09j3g2 hepatitis c	772	74.5	6.2	377	2	Q4R2M8_VARH1	Q4R2M8 vargula h11
700	75	6.3	3010	2	09J3G5_9HEPC	09j3g5 hepatitis c	773	74.5	6.2	377	2	Q4R2P2_VARH1	Q4R2P2 vargula h11
701	75	6.3	3010	2	09Q1Y7_9HEPC	09q1y7 hepatitis c	774	74.5	6.2	377	2	Q4R2A2_VARH1	Q4R2A2 vargula h11
702	75	6.3	3010	2	09Q1Y8_9HEPC	09q1y8 hepatitis c	775	74.5	6.2	377	2	Q4R2E7_VARH1	Q4R2E7 vargula h11
703	75	6.3	3010	2	P97068_9ENTR	P97068 salmonella	776	74.5	6.2	377	2	Q6DIV8_BRANA	Q6div8 brasica na
704	74.5	6.2	174	2	08EPH9_OCEIH	08eph9 oceanobacil	777	74.5	6.2	378	2	CYB_OCHER	Q9gb4 ochocona pr
705	74.5	6.2	179	2	08EPH9_OCEIH	P71253 escherichia	778	74.5	6.2	379	1	Q6ELW8_OCHPR	Q6elw8 ochocona pr
706	74.5	6.2	180	2	P71253_ECOLI	Q9gat5 ochocona th	779	74.5	6.2	379	2	Q8WB05_APLRU	Q8wb05 apidodonta
707	74.5	6.2	227	2	09GAT5_OCHTU	Q9gat5 ochocona cu	780	74.5	6.2	379	2	Q8WB05_APLRU	Q8wb05 chaetodipus
708	74.5	6.2	227	2	09GAT5_OCHTU	Q9gat5 ochocona cu	781	74.5	6.2	379	2	Q9B9E3_CHAPN	Q9b9e3 microomop
709	74.5	6.2	227	2	088WC7_LACPL	088wc7 lactobacill	782	74.5	6.2	392	2	09LCN4_MICOL	09lcn4 arabisdops
710	74.5	6.2	276	2	09R905_RHIME	Q9r95 rhizobium m	783	74.5	6.2	442	2	09A4I3_CANAL	Q59yv2 candida alb
711	74.5	6.2	280	2	06WIF6_SYNP8	Q6wif6 synechococ	784	74.5	6.2	450	2	059YV2_CANAL	Q59yv2 bacillus li
712	74.5	6.2	290	2	06SEU1_9BACT	Q6seu1 uncultured	785	74.5	6.2	458	2	065MD8_BACLD	Q65md8 bacillus li
713	74.5	6.2	298	2	06BMD3_DEBHA	Q6bwd3 debaryomyce	786	74.5	6.2	471	1	5HT2A_RAT	P14842 rattus norv
714	74.5	6.2	298	2	05LEN3_ENTHI	Q5len3 entamoeba h	787	74.5	6.2	471	1	Q4U3W9_MESAU	Q4u3w9 mesocricetu
715	74.5	6.2	313	2	08RTK6_THETN	Q8r7k6 thermoaer	788	74.5	6.2	473	2	09K5Y9_BACHD	Q9k5y9 bacillus ha
716	74.5	6.2	335	2	09WKS7_THEMA	Q9wks7 thermotoga	789	74.5	6.2	488	2	06OU71_ASPTU	Q6ou71 aspergillus
717	74.5	6.2	346	2	05FMK7_LACAC	Q5fmk7 lactobacill	790	74.5	6.2	500	2	024348_SORBI	Q24348 sorghum bic
718	74.5	6.2	355	1	CX3C1_HUMAN	P99238 homo sapien	791	74.5	6.2	523	2	05UBD4_CRYNE	Q5ubd4 cryptococcu
719	74.5	6.2	358	2	Q5WHM9_BACSK	Q5whm9 bacillus cl	792	74.5	6.2	523	2	05K102_CRYNE	Q5k102 cryptococcu
720	74.5	6.2	364	2	08IDY2_PLAUF	Q8idy2 plasmodium	793	74.5	6.2	540	2	06G6G5_ARATH	Q6g6g5 arabidops
721	74.5	6.2	377	2	Q76W3_VARRH	Q76w3 vargula h11	794	74.5	6.2	548	2	05ZER6_MAGGR	Q5zer6 magnaporthe
722	74.5	6.2	377	2	Q4R2N5_VARH1	Q4r2n5 vargula h11	795	74.5	6.2	562	2	08N2S3_HUMAN	Q8n2s3 homo sapien
723	74.5	6.2	377	2	Q4R2N4_VARH1	Q4r2n4 vargula h11	796	74.5	6.2	574	2	022454_WHEAT	Q22454 triticum ae
724	74.5	6.2	377	2	Q4R2K8_VARH1	Q4r2k8 vargula h11	797	74.5	6.2	594	2	Q4MUQ1_ASPTU	Q4muq1 aspergillus
725	74.5	6.2	377	2	Q4R2K5_VARH1	Q4r2k5 vargula h11	798	74.5	6.2	597	2	Q4R2N1_ASPTU	Q4r2n1 vargula h11
726	74.5	6.2	377	2	Q4R2K3_VARH1	Q4r2k3 vargula h11	799	74.5	6.2	618	1	Q9VD40_DROME	Q9vd40 drosophila
727	74.5	6.2	377	2	Q4R2K2_VARH1	Q4r2k2 vargula h11	800	74.5	6.2	697	2	YKRA4_YEAST	Q4pcy9 uetliago ma
728	74.5	6.2	377	2	Q4R2K1_VARH1	Q4r2k1 vargula h11	801	74.5	6.2	793	2	Q4PCY9_USTMA	Q4pcy9 corynebacte
729	74.5	6.2	377	2	Q4R2J3_VARH1	Q4r2j3 vargula h11	802	74.5	6.2	848	2	08VVK9_CORGL	Q8vvk9 vibrio vuln
730	74.5	6.2	377	2	Q4R2I1_VARH1	Q4r2i1 vargula h11	803	74.5	6.2	990	1	FTSK_VIBVU	Q4ub87 yelleria a
731	74.5	6.2	377	2	Q4R2H9_VARH1	Q4r2h9 vargula h11	804	74.5	6.2	1022	2	Q4UBR7_THEAN	Q722c1 trypanosoma
732	74.5	6.2	377	2	Q4R2H6_VARH1	Q4r2h6 vargula h11	805	74.5	6.2	1033	2	Q722C1_TRYBB	Q722c0 cylliposoma
733	74.5	6.2	377	2	Q4R2G0_VARH1	Q4r2g0 vargula h11	806	74.5	6.2	1034	2	Q722C0_9TRYP	Q94447 calliphora
734	74.5	6.2	377	2	Q4R2F7_VARH1	Q4r2f7 vargula h11	807	74.5	6.2	1193	2	094447_CALTY	Q91y66 arabidops
735	74.5	6.2	377	2	Q4R2E3_VARH1	Q4r2e3 vargula h11	808	74.5	6.2	1401	2	061PW5_CAEBR	Q61pw5 caenorhabdi
736	74.5	6.2	377	2	Q4R2D6_VARH1	Q4r2d6 vargula h11	809	74.5	6.2	1520	2	08T6B7_DICDI	Q8t6b7 dictyosteli
737	74.5	6.2	377	2	Q4R2C9_VARH1	Q4r2c9 vargula h11	810	74.5	6.2	1534	2	054TV1_DICDI	Q54tv1 dictyosteli
738	74.5	6.2	377	2	Q4R2C4_VARH1	Q4r2c4 vargula h11	811	74.5	6.2	1559	2	Q7S0S1_NEUCR	Q7s0s1 neurospora
739	74.5	6.2	377	2	Q4R2B4_VARH1	Q4r2b4 vargula h11	812	74.5	6.2	1640	2	054Z25_DICDI	Q54z25 dictyosteli
740	74.5	6.2	377	2	Q4R2B3_VARH1	Q4r2b3 vargula h11	813	74.5	6.2	1808	2	091YX6_ARATH	Q91yx6 arabidops
741	74.5	6.2	377	2	Q4R2B6_VARH1	Q4r2b6 vargula h11	814	74.5	6.2	1837	2	08IKP1_PLAUF	Q8ikp1 plasmodium
742	74.5	6.2	377	2	Q4R2B5_VARH1	Q4r2b5 vargula h11	815	74.5	6.2	3010	2	091AN0_9HEPC	Q91an0 hepatitis c
743	74.5	6.2	377	2	Q4R2B9_VARH1	Q4r2b9 vargula h11	816	74	6.2	124	2	08KC46_CHLIE	Q8kc46 chlorobium
744	74.5	6.2	377	2	Q4R289_VARH1	Q4r289 vargula h11	817	74	6.2	156	2	Q8W272_HUMAN	Q8w272 homo sapien
745	74.5	6.2	377	2	Q4R288_VARH1	Q4r288 vargula h11	818	74	6.2	167	2	Q5VHX0_EAV	Q5vhx0 equine arte
746	74.5	6.2	377	2	Q4R286_VARH1	Q4r286 vargula h11	819	74	6.2	173	2	05HCD2_EHRRW	Q5hcd2 ehrllichia r
747	74.5	6.2	377	2	Q4R285_VARH1	Q4r285 vargula h11	820	74	6.2	220	2	091S82_CORO	Q91s82 avian iftec
748	74.5	6.2	377	2	Q4R273_VARH1	Q4r273 vargula h11	821	74	6.2	225	2	088Y70_LACPL	Q88y70 lactobacill
749	74.5	6.2	377	2	Q4R268_VARH1	Q4r268 vargula h11	822	74	6.2	230	2	Q0BS2_ARCFU	Q0b892 archaeoglob
750	74.5	6.2	377	2	Q4R254_VARH1	Q4r254 vargula h11	823	74	6.2	231	1	028892_ARCFU	Q28892 dictyosteli
751	74.5	6.2	377	2	Q4R244_VARH1	Q4r244 vargula h11	824	74	6.2	238	2	06HER1_BACIL	Q6her1 bacillus th
752	74.5	6.2	377	2	Q4R223_VARH1	Q4r223 vargula h11	825	74	6.2	255	2	066483_EAV	Q66483 equine arte
753	74.5	6.2	377	2	Q4R222_VARH1	Q4r222 vargula h11	826	74	6.2	278	2	06CUI8_KLUTLA	Q6cu18 kluyveromyc
754	74.5	6.2	377	2	Q4R201_VARH1	Q4r201 vargula h11	827	74	6.2	279	2	Q4XPR5_PLACH	Q4xpr5 mycoplasma
755	74.5	6.2	377	2	Q4R126_VARH1	Q4r126 vargula h11	828	74	6.2	286	1	POTB_MYCPN	P75058 pseudoplasma
756	74.5	6.2	377	2	Q4R126_VARH1	Q4r126 vargula h11	829	74	6.2	291	1	Q669G8_YERPS	Q669g8 yersinia ps
757	74.5	6.2	377	2	Q4R124_VARH1	Q4r124 vargula h11	830	74	6.2	295	1	CYOE_PSEPU	Q9wv5 pseudomonas
758	74.5	6.2	377	2	Q4R1Y1_VARH1	Q4r1y1 vargula h11	831	74	6.2	297	2	06S4W3_PSEPU	Q6s4w3 pseudomonas
759	74.5	6.2	377	2	Q4R1X3_VARH1	Q4r1x3 vargula h11	832	74	6.2	297	2	Q61BC3_CAEBR	Q61bc3 caenorhabdi
760	74.5	6.2	377	2	Q4R1W6_VARH1	Q4r1w6 vargula h11	833	74	6.2	300	1	NU2M_ASCSU	P24877 aecetis buu

835	74	6.2	312	1	PYR8_AERPE	O9yhd4_aeropyrum p	908	73.5	6.2	180	2	P71257_ECOLI	P71257_esch
836	74	6.2	312	2	O9CH74_LACIA	O9ch74_lactococcus	909	73.5	6.2	180	2	P75018_ECOLI	P75018_esch
837	74	6.2	315	2	O710S2_SPAXH	O710s2_spatax leuc	910	73.5	6.2	199	2	O8DVR3_STPMU	O8dvr3_streptoc
838	74	6.2	321	2	O8M6V0_9MATH	O8m6v0_ligilopsis j	911	73.5	6.2	216	1	Y2036_AQUAE	O67827_aquifex
839	74	6.2	324	2	O8DVZ6_STRMU	O8dvz6_streptococ	912	73.5	6.2	217	2	O4TEY9_TETNG	O4tey9_tetradon
840	74	6.2	333	2	O4FNS1_9RICK	O4fns1_candidatus	913	73.5	6.2	226	2	O5WAP0_9CORA	O5wap0_avian infec
841	74	6.2	339	2	O6IRG9_CABER	O6irg9_caenorhabdi	914	73.5	6.2	226	2	O9J0X1_9CORA	O9j0x1_avian infec
842	74	6.2	342	2	O621V1_CABER	O621v1_caenorhabdi	915	73.5	6.2	267	2	O50261_ENTHI	O50261_entamoeba h
843	74	6.2	349	1	I10R2_MOUSE	O621v1_mus muscicu	916	73.5	6.2	270	2	O8HIV6_PERLO	O8hiv6_perognathus
844	74	6.2	350	1	MTRIA1_HUMAN	P48039_homo sapien	917	73.5	6.2	270	2	O8HBP0_PERLO	O8hbp0_perognathus
845	74	6.2	351	2	O8VHM7_MOUSE	O8vhm7_mus muscicu	918	73.5	6.2	274	2	O95L51_CAPHI	O95l51_capra hircu
846	74	6.2	354	2	O6SUI3A_MANSU	O6sui3a_mannheimia	919	73.5	6.2	278	2	O4C0C8_SULAC	O4c0c8_sulfolobus
847	74	6.2	357	2	O5FV66_MEDPR	O5fv66_medicago tr	920	73.5	6.2	286	2	O4HS16_CAMP	O4hs16_campylobact
848	74	6.2	361	2	O6ALD9_9ARCH	O6ald9_uncultured	921	73.5	6.2	298	2	O6Z2T3_ORYSA	O6z2t3_oryza sativ
849	74	6.2	379	1	CYB_THOMO	O8wex2_thomomys mo	922	73.5	6.2	303	2	O5J3K5_RAT	O5j3k5_rattus norv
850	74	6.2	379	2	O48002_THOMO	O48002_thomomys mo	923	73.5	6.2	304	2	O5NP42_ZYMO	O5np42_zymomonas m
851	74	6.2	379	2	O48003_THOMO	O48003_thomomys mo	924	73.5	6.2	305	2	O4POE6_USTWA	O4poe6_usuliago ma
852	74	6.2	379	2	O47980_THORO	O47980_thomomys bo	925	73.5	6.2	318	2	O55895_SYNY3	O55895_synecocyst
853	74	6.2	379	2	O8WEX5_THORA	O8wex5_thomomys ta	926	73.5	6.2	338	1	YVAD_BACSU	P37520_bacillus su
854	74	6.2	379	2	O8HHJ7_THORO	O8hhj7_thomomys bo	927	73.5	6.2	355	2	O4J826_SULAC	O4j826_sulfolobus
855	74	6.2	379	2	O59J07_9SCIU	O59j07_plecomys vo	928	73.5	6.2	360	2	O8UWM8_BRABE	O8uwm8_brachydanio
856	74	6.2	380	2	O74XK0_LACCU	O74xb0_lactobacilli	929	73.5	6.2	367	2	O64BD6_9ARCH	O64bd6_uncultured
857	74	6.2	381	1	CYB_PSENI	O35553_pseudantech	930	73.5	6.2	373	2	O5F117_LACAC	O5f117_lactobacilli
858	74	6.2	382	2	O5R7A1_PONPY	O5r7a1_pongo pygma	931	73.5	6.2	379	1	CYB_PHOGR	O5f117_lactobacilli
859	74	6.2	386	2	O6GAR1_STAS	O6gar1_staphylococ	932	73.5	6.2	379	2	O9G3M8_OCHCU	O9g3m8_ochotona li
860	74	6.2	386	2	O6G168_STAPK	O6g168_staphylococ	933	73.5	6.2	379	2	O588N8_SCILI	O588n8_sciurus lis
861	74	6.2	396	2	O5HH70_STAC	O5hh70_staphylococ	934	73.5	6.2	379	2	O508U7_PERRA	O508u7_petrognathus
862	74	6.2	396	2	O7A6D3_STAN	O7a6d3_staphylococ	935	73.5	6.2	379	2	O508U0_9RODE	O508u0_petrognathus
863	74	6.2	396	2	O8NXC4_STAM	O8nxc4_staphylococ	936	73.5	6.2	380	1	CYB_STRPU	P15547_strongyloce
864	74	6.2	397	2	O99V76_STAM	O99v76_staphylococ	937	73.5	6.2	384	1	OPGC_SALTY	O8zq27_salmonella
865	74	6.2	397	2	O4Z254_PLABE	O4z254_plasmodium	938	73.5	6.2	384	1	OPGC_SALTY	O8zq27_salmonella
866	74	6.2	398	2	O5NEU8_FRATT	O5neu8_francisella	939	73.5	6.2	385	2	P94442_BACSU	O94k42_bacillus su
867	74	6.2	410	2	O4R103_TETNG	O4r103_tetradodon n	940	73.5	6.2	387	2	O9KXU2_9SPHN	O9kxu2_sphingomon
868	74	6.2	418	2	O6OFC5_LEGPN	O6ofc5_legionella	941	73.5	6.2	387	2	O7WVX5_PORGI	O7wvx5_porphryomon
869	74	6.2	418	2	O6OFC5_LEGPN	O6ofc5_legionella	942	73.5	6.2	389	1	OXYR_BOVIN	O56494_macaca mula
870	74	6.2	418	2	O6OFC7_LEGPN	O6ofc7_legionella	943	73.5	6.2	391	1	OXYR_BOVIN	O56494_macaca mula
871	74	6.2	436	2	O5QZG8_IDILIO	O5qzg8_idiomarina	944	73.5	6.2	397	2	O8Z2F7_ENTRA	O8z2f7_enterococ
872	74	6.2	442	2	O9CEG6_IACIA	O9ceg6_lactococcus	945	73.5	6.2	397	2	O7V140_PROMP	O7v140_promelioc
873	74	6.2	452	2	O4NJC7_9MICC	O4njc7_arthrobacte	946	73.5	6.2	409	2	O928T3_LISIN	O928t3_listeria in
874	74	6.2	457	2	O8R8Z7_THERN	O8r8z7_thermoanaer	947	73.5	6.2	413	2	O8PKX7_XANAC	O8pkx7_xanthomonas
875	74	6.2	471	2	O9S2G7_STROMC	O9s2g7_streptomyce	948	73.5	6.2	421	2	O6D6K1_ERMCT	O6d6k1_erwinia car
876	74	6.2	485	2	O4Q1F4_LEINA	O4q1f4_leishmania	949	73.5	6.2	442	2	O8GZJ4_ARATH	O8gzj4_arabidopsis
877	74	6.2	485	2	O9XVK0_CABEL	O9xvk0_caenorhabdi	950	73.5	6.2	442	2	O9XJ07_ARATH	O9xj07_arabidopsis
878	74	6.2	487	2	O23384_ARATH	O23384_arabidopsis	951	73.5	6.2	491	1	VIE1_HCVYA	P13282_human cytom
879	74	6.2	493	2	O9EVJ7_FLALTU	O9evj7_flavobacter	952	73.5	6.2	491	1	O6SW28_HCVY	O6sw28_human cytom
880	74	6.2	503	2	O6M052_METMP	O6m052_methanococ	953	73.5	6.2	518	2	O7RT44_PLAYO	O7rt44_plasmodium
881	74	6.2	505	2	O4NS89_9DELT	O4ns89_aeromonycob	954	73.5	6.2	518	2	O64WY6_BACPR	O64wy6_bacteroides
882	74	6.2	528	2	O70109_KUULA	O70109_kluyteromyc	955	73.5	6.2	523	2	O5LQ29_BACPR	O5lq29_bacteroides
883	74	6.2	530	2	O51FL8_ENTHI	O51fl8_entamoeba h	956	73.5	6.2	523	2	O7PVT1_ANODA	O7pvt1_anopheles g
884	74	6.2	540	2	O6LFP3_PLAF7	O6lfp3_plasmodium	957	73.5	6.2	555	2	O8VZE2_ARATH	O8vze2_arabidopsis
885	74	6.2	581	2	O6F1I6_CANGA	O6f1i6_candida gla	958	73.5	6.2	557	2	O5ATP6_EMENT	O5atp6_aspergillus
886	74	6.2	584	2	O5KA08_CRYNE	O5ka08_cryptococcu	959	73.5	6.2	574	2	O93990_CANAL	O93990_candida alb
887	74	6.2	599	2	O5KA09_CRYNE	O5ka09_cryptococcu	960	73.5	6.2	574	2	O5A4P9_CANAL	O5a4p9_candida alb
888	74	6.2	650	2	O9S6S6_9ACT	O9s6s6_lactococcus	961	73.5	6.2	574	2	O6DFJ5_XENLA	O6dfj5_xenopus lae
889	74	6.2	681	2	O4FIS7_9GAMM	O4fis7_psychrobact	962	73.5	6.2	607	2	O5C841_CRYHO	O5c841_cryptospori
890	74	6.2	841	2	O6FNV6_CANGA	O6fnv6_candida gla	963	73.5	6.2	634	1	KUP_XYTFA	O9pcr8_xylotella fas
891	74	6.2	842	2	O9AIP1_CARRU	O9aip1_carsonella	964	73.5	6.2	634	1	MUTL_BACHD	O9paci_bacillus ha
892	74	6.2	846	2	O93U47_CARRU	O93u47_carsonella	965	73.5	6.2	640	1	APRN_ENTHI	P20301_entamoeba h
893	74	6.2	892	2	O8TGR2_CANAL	O8tgr2_candida alb	966	73.5	6.2	640	1	O8THI1_METAC	O8thi1_methanosarc
894	74	6.2	943	2	O4IM19_GIBZE	O4im19_glibberella	967	73.5	6.2	653	2	O88468_CORAM	O88468_corynebacte
895	74	6.2	1123	2	O9SE99_ARATH	O9se99_arabidopsis	968	73.5	6.2	661	2	O5IWR5_GLYGR	O5iwr5_glycycaria gr
896	74	6.2	1123	2	O9SPU7_ARATH	O9spu7_arabidopsis	969	73.5	6.2	715	2	O16531_CABEL	O16531_caenorhabdi
897	74	6.2	1216	2	O5S1S2_CRYNE	O5s1s2_cryptococcu	970	73.5	6.2	846	2	O93J05_CARRU	O93j05_carsonella
898	74	6.2	1216	2	O5KCK7_CRYNE	O5kck7_cryptococcu	971	73.5	6.2	859	2	O4Y0Y1_PLABE	O4y0y1_plasmodium
899	74	6.2	3010	2	O913V3_9HEPC	O913v3_hepatitis c	972	73.5	6.2	881	2	O5ZM00_CHICK	O5zm00_gallus galli
900	74	6.2	3010	2	O9DTR8_9HEPC	O9dtr8_hepatitis c	973	73.5	6.2	992	2	O51315_ENTHI	O51315_entamoeba h
901	74	6.2	3010	2	O9J3H6_9HEPC	O9j3h6_hepatitis c	974	73.5	6.2	1006	2	O4YH36_PLABE	O4yh36_plasmodium
902	74	6.2	3010	2	O9QIY1_9HEPC	O9qiyl_hepatitis c	975	73.5	6.2	1049	2	O6FTY2_CANGA	O6fty2_candida gla
903	74	6.2	3010	2	O9QIY2_9HEPC	O9qiyl2_hepatitis c	976	73.5	6.2	1095	2	O9C7H5_ARATH	O9c7h5_arabidopsis
904	73.5	6.2	120	2	O9SKA6_ARATH	O9ska6_arabidopsis	977	73.5	6.2	1174	2	O7M006_9CORA	O7m006_murine hepa
905	73.5	6.2	153	2	O9ZKX3_RHIME	O9zkx3_rhizobium m	978	73.5	6.2	1175	2	O4H0G2_CAMCO	O4hdg2_campylobact
906	73.5	6.2	180	2	O8ZKX3_PYRAE	O8zkx3_pyrobaculum	979	73.5	6.2	1277	2	O76G00_CIOIN	O76g00_ciona intes
907	73.5	6.2	180	2	P71251_ECOLI	P71251_esch	980	73.5	6.2				

981	73.5	6.2	1287	2	Q7YU59_DROME	Q7YU59_drosophila	1054	73	6.1	446	2	Q8H9B3_BRACH	Q8H9B3_brassica ca
982	73.5	6.2	1287	2	Q9U5W1_DROME	Q9U5W1_drosophila	1055	73	6.1	450	1	VGLM_EHY1B	PG8948 equine herp
983	73.5	6.2	1287	2	Q9VU24_DROME	Q9VU24_drosophila	1056	73	6.1	450	2	Q6S6T2_GALPH	Q6S6T2 equine herpe
984	73.5	6.2	1292	2	Q9A1H0_CARRU	Q9A1H0_carsonella	1057	73	6.1	453	2	Q943I7_CAEEL	Q943I7_caenorhabdi
985	73.5	6.2	1476	2	Q965D3_DICDI	Q965D3_dicyosbati	1058	73	6.1	461	2	Q9R923_STRPN	Q9R923_streptococ
986	73.5	6.2	1545	2	Q8GUE5_ORYSA	Q8GUE5_oryza sativ	1059	73	6.1	461	2	Q4K0U6_STRPN	Q4K0U6_streptococ
987	73.5	6.2	2666	2	Q6FW99_CANGA	Q6FW99_candida gla	1060	73	6.1	470	2	Q54PF0_DICDI	Q54PF0_dicyosbati
988	73.5	6.2	3007	2	Q4SSR8_TETNG	Q4SSR8_tetradom n	1061	73	6.1	474	2	Q94C17_ARATH	Q94C17_arabidopsis
989	73.5	6.2	3010	2	Q9DTE6_9HEPC	Q9DTE6_hepatitis c	1062	73	6.1	481	2	Q4K4Z1_PSEFS	Q4K4Z1_pseudomonas
990	73.5	6.2	3381	2	Q8IDK4_ILAP7	Q8IDK4_plasmodium	1063	73	6.1	487	2	Q7MBAS_PHOIL	Q7MBAS_photorhabdu
991	73.5	6.2	4470	2	Q66WNS_9CORO	Q66WNS_murine hepa	1064	73	6.1	488	2	Q4HRT1_CAMUP	Q4HRT1_campylobac
992	73.5	6.2	7176	1	RIAB_CVMAS	RIAB342 m replicase	1065	73	6.1	494	1	KCNF1_HUMAN	Q9H3HO homo sapien
993	73.5	6.2	7178	1	Q66WNS_9CORO	Q66WNS_murine hepa	1066	73	6.1	494	2	Q85UJ3_HUMAN	Q85UJ3 homo sapien
994	73	6.1	114	2	Q75XAT_HELPY	Q75XAT_helicobacte	1067	73	6.1	509	2	Q5CUK7_CRYEV	Q5CUK7_cryptospori
995	73	6.1	114	2	Q9ZLUZ_HELPY	Q9ZLUZ_helicobacte	1068	73	6.1	510	2	Q27072_TAESOL	Q27072_taeia soli
996	73	6.1	138	2	Q97777_ELEMA	Q97777_eiephas max	1069	73	6.1	520	2	Q5KWR7_GEOKA	Q5KWR7_geobacillus
997	73	6.1	140	2	Q64145_TMURI	Q64145_rattus sp.	1070	73	6.1	546	2	Q5EAY8_KENNA	Q5EAY8_xenopus lae
998	73	6.1	145	2	Q9UXB0_SULSO	Q9UXB0_sulfolobus	1071	73	6.1	553	2	Q59PV9_CANAL	Q59PV9_candida alb
999	73	6.1	155	2	Q7VJPI_HELPH	Q7VJPI_helicobacte	1072	73	6.1	553	2	Q9ZUJ5_HELPY	Q9ZUJ5_helicobacte
1000	73	6.1	156	2	Q81510_9HEPC	Q81510_hepatitis c	1073	73	6.1	556	2	Q7Q2U9_GIALA	Q7Q2J9_giardia lam
1001	73	6.1	156	2	Q81522_9HEPC	Q81522_hepatitis c	1074	73	6.1	616	2	Q6BIQ1_DEBHA	Q6BIQ1_debaryomyce
1002	73	6.1	156	2	Q81537_9HEPC	Q81537_hepatitis c	1075	73	6.1	623	2	Q4RMH4_TETNG	Q4RMH4_tetradom n
1003	73	6.1	163	2	Q80RY8_9CORO	Q80RY8_avian infec	1076	73	6.1	635	2	Q86X77_HUMAN	Q86X77_homo sapien
1004	73	6.1	220	2	Q72240_BACCI	Q72240_bacillus ce	1077	73	6.1	643	2	Q7NBK6_MYCGA	Q7NBK6_mycoplasma
1005	73	6.1	223	2	VMEI_IBVG	Q910E2_avian infec	1078	73	6.1	668	2	Q9ALX8_BURPS	Q9ALX8_burkholderi
1006	73	6.1	223	2	Q91597_9CORO	Q91597_avian infec	1079	73	6.1	668	2	Q63161_BURPS	Q63161_burkholderi
1007	73	6.1	226	2	Q7T9P6_9CORO	Q7T9P6_avian infec	1080	73	6.1	676	2	Q9VFJ1_DROME	Q9VFJ1_drosophila
1008	73	6.1	238	1	BYRF_BACCR	Q81966_bacillus ce	1081	73	6.1	703	2	Q4MSR5_CAEEL	Q4MSR5_caenorhabdi
1009	73	6.1	238	2	Q4MU75_BACCE	Q4MU75_bacillus ce	1082	73	6.1	716	2	Q59LX3_CANAL	Q59LX3_candida alb
1010	73	6.1	238	2	Q636E3_BACC2	Q636E3_bacillus ce	1083	73	6.1	788	1	FTSK_STANM	FTSK_STANM
1011	73	6.1	238	2	Q73216_BACCI	Q73216_bacillus ce	1084	73	6.1	789	1	Q6GHP9_STAAR	Q6GHP9_staphylococ
1012	73	6.1	249	2	Q9FDU6_STRPY	Q9FDU6_streptococ	1085	73	6.1	789	2	Q5HGFS_STAAC	Q5HGFS_staphylococ
1013	73	6.1	255	2	P87639_EAV	P87639_equine arte	1086	73	6.1	792	2	Q5Z6J8_ORYSA	Q5Z6J8_oryza sativ
1014	73	6.1	255	2	Q9YNU0_EAV	Q9YNU0_equine arte	1087	73	6.1	805	2	Q7UQF9_RHOBA	Q7UQF9_rhodospirill
1015	73	6.1	260	2	Q7QNI9_ANOGA	Q7QNI9_anophelae g	1088	73	6.1	832	2	Q6KX78_PICTO	Q6KX78_picrophilus
1016	73	6.1	264	2	Q8DAQ9_VIBVU	Q8DAQ9_vibriol vuln	1089	73	6.1	844	2	Q9AVX8_GUTTH	Q9AVX8_gutthardia
1017	73	6.1	264	2	Q6TY95_VIBVY	Q6TY95_xiphinema a	1091	73	6.1	861	2	PXD2_MOUSE	Q8BPR6_mus musculu
1018	73	6.1	279	2	Q6TY95_9BILA	P24889_caenorhabdi	1092	73	6.1	966	1	Q8BPR6_MOUSE	Q8BPR6_mus musculu
1019	73	6.1	282	1	NUZM_CAEEL	Q6G9W4_staphylococ	1093	73	6.1	966	2	Q7TSI7_MOUSE	Q7TSI7_mus musculu
1020	73	6.1	290	2	Q6G9W4_STAAS	Q6G9W4_staphylococ	1094	73	6.1	971	2	Q6O3J7_HUMAN	Q6O3J7_homo sapien
1021	73	6.1	290	2	Q5HGJ3_STAAM	Q5HGJ3_staphylococ	1095	73	6.1	1035	2	Q967W1_SCHMA	Q967W1_schistosoma
1022	73	6.1	290	2	Q8NXU0_STAAM	Q8NXU0_staphylococ	1096	73	6.1	1035	2	Q9LPE2_ARATH	Q9LPE2_arabidopsis
1023	73	6.1	294	2	Q4X7M3_PLACH	Q4X7M3_plasmodium	1097	73	6.1	1111	2	Q86FP2_CAEEL	Q86FP2_caenorhabdi
1024	73	6.1	294	2	Q4X747_PLACH	Q4X747_plasmodium	1098	73	6.1	1127	2	Q9N3J3_CAEEL	Q9N3J3_caenorhabdi
1025	73	6.1	295	2	Q5AZG6_EMENT	Q5AZG6_aepereyillu	1099	73	6.1	1156	2	Q4MGW4_ASPTU	Q4MGW4_aepereyillu
1026	73	6.1	295	2	Q8VUQ2_PSEBU	Q8VUQ2_pseudomonas	1100	73	6.1	1268	2	Q553T5_DICDI	Q553T5_dicyosbati
1027	73	6.1	295	2	Q88FN3_PSEBU	Q88FN3_pseudomonas	1101	73	6.1	1268	2	Q8RUT3_STIAN	Q8RUT3_stigmantella
1028	73	6.1	303	2	Q94EJO_ARATH	Q94EJO_arabidopsis	1102	73	6.1	1931	2	Q7PZM7_ANOGA	Q7PZM7_anophelae g
1029	73	6.1	314	2	Q8ESH3_OCEIH	Q8ESH3_oceanobacil	1103	73	6.1	1951	2	P88803_9HEPC	P88803_hepatitis c
1030	73	6.1	322	2	Q9H6T9_HUMAN	Q9H6T9_homo sapien	1104	73	6.1	3010	2	Q9J3G1_9HEPC	Q9J3G1_hepatitis c
1031	73	6.1	326	2	Q99NR7_MUSAV	Q99NR7_muscardinus	1105	73	6.1	3013	2	Q9QIX9_9HEPC	Q9QIX9_hepatitis c
1032	73	6.1	335	2	Q8SM78_ENCCU	Q8SM78_encephalito	1106	73	6.1	3013	2	Q9QIY0_9HEPC	Q9QIY0_hepatitis c
1033	73	6.1	339	1	SRG7_CAEEL	PS4123_caenorhabdi	1107	73	6.1	3013	2	Q9QIY0_9HEPC	Q9QIY0_hepatitis c
1034	73	6.1	340	2	Q9N2T2_CAEEL	Q9N2T2_caenorhabdi	1108	73	6.1	3013	2	Q9QIY0_9HEPC	Q9QIY0_hepatitis c
1035	73	6.1	343	2	Q7YFUO_9HYME	Q7YFUO_myrmica sul	1109	73	6.1	6875	2	Q287J3_RABIT	Q287J3_oryctolagus
1036	73	6.1	343	2	Q85A87_UMASC	Q85A87_unia scopari	1110	73	6.1	105	2	Q5ALK7_CANAL	Q5ALK7_candida alb
1037	73	6.1	348	1	Q9TDA9_9SMEG	Q9TDA9_crymolebias	1111	73	6.1	156	2	Q81516_9HEPC	Q81516_hepatitis c
1038	73	6.1	364	1	GHSR_MOUSE	Q99P50_mus musculu	1112	73	6.1	156	2	Q81519_9HEPC	Q81519_hepatitis c
1039	73	6.1	364	1	GHSR_RAT	Q08725_rattus norv	1113	73	6.1	167	2	Q5KIY4_CRYNE	Q5KIY4_cryptococcu
1040	73	6.1	375	2	Q86NCO_CAEEL	Q86NCO_caenorhabdi	1114	73	6.1	173	2	Q9MDI7_EAV	Q9MDI7_equine arte
1041	73	6.1	378	2	Q7OEG5_9RODE	Q7OEG5_saccosotomus	1115	73	6.1	174	2	P97065_9ENTR	P97065_salmonella
1042	73	6.1	378	2	Q7OEG4_9RODE	Q7OEG4_saccosotomus	1116	73	6.1	180	2	P71252_ECOLI	P71252_eecherichia
1043	73	6.1	379	1	CYB_CRAFU	Q8wdv6_cratogeomys	1117	73	6.1	180	2	P71254_ECOLI	P71254_eecherichia
1044	73	6.1	379	2	Q8MDV7_CRAFY	Q8MDV7_cratogeomys	1118	73	6.1	180	2	P71255_ECOLI	P71255_eecherichia
1045	73	6.1	379	2	Q34099_CRAFU	Q34099_cratogeomys	1119	73	6.1	180	2	P71256_ECOLI	P71256_eecherichia
1046	73	6.1	379	2	Q698Q2_CRAFU	Q698Q2_cratogeomys	1120	73	6.1	180	2	P71258_ECOLI	P71258_eecherichia
1047	73	6.1	383	1	Q9GL20_CYNBP	Q9GL20_cynopterus	1121	73	6.1	180	2	P71259_ECOLI	P71259_eecherichia
1048	73	6.1	391	2	Y450_BUCAP	Q8K939_buchnera ap	1122	73	6.1	180	2	P71260_ECOLI	P71260_eecherichia
1049	73	6.1	394	2	Q6EE89_LATCH	Q6EE89_lactimeria c	1123	73	6.1	180	2	P71261_ECOLI	P71261_eecherichia
1050	73	6.1	399	2	Q6LOJ3_PICTO	Q6LOJ3_picrophilus	1124	73	6.1	191	2	O55TJ2_CRYNE	O55TJ2_cryptococcu
1051	73	6.1	401	2	Q6KZX3_PICTO	Q6KZX3_picrophilus	1125	73	6.1	208	2	O8U4P0_CYRRU	O8U4P0_pyrococcu
1052	73	6.1	412	2	Q61M38_CAEER	Q61M38_caenorhabdi	1126	73	6.1	208	2	O63447_ECHDI	O63447_echinocrix
1053	73	6.1	437	2	Q4YNS0_PLABE	Q4YNS0_plasmodium	1126	73	6.1	208	2	Q7J7L2_ECHDI	Q7J7L2_echinocrix



1127	72.5	6.1	209	2	Q7J7T60_ECHDI	Q7J710_echiotrix	1200	72.5	6.1	457	2	Q6P822_XENIR	Q6P822 xenopus tro
1128	72.5	6.1	209	2	Q8GZ10_ARATH	Q8GZ10 arabidopsis	1201	72.5	6.1	478	2	Q970D2_SUITO	Q970D2 silicolobus
1129	72.5	6.1	209	2	Q49834_MYCLE	Q49834 mycobacteri	1202	72.5	6.1	488	2	Q4HEC1_CAMCO	Q4HEC1 campylobact
1130	72.5	6.1	210	2	Q7J7L9_ECHDI	Q7J719 echiotrix	1203	72.5	6.1	488	2	Q4HLMO_CAMLA	Q4HLMO camylobact
1131	72.5	6.1	211	2	Q7J7L3_ECHDI	Q7J713 echiotrix	1204	72.5	6.1	491	1	Q6SWL8_HCMV	Q6SWL8 human cytom
1132	72.5	6.1	214	2	Q63950_ECHDI	Q63950 echiotrix	1205	72.5	6.1	499	1	Q6V1N1_AQULP	Q6V1N1 aquilex aeo
1133	72.5	6.1	217	2	Q9XMX7_OCHPR	Q9XMX7 ochotona pr	1206	72.5	6.1	505	2	Q8ORY6_9BETA	Q8ORY6 pongine her
1134	72.5	6.1	224	2	Q8RGE6_FUSNN	Q8RGE6 fusobacteri	1207	72.5	6.1	513	1	PACR_BOVIN	Q29627 bos taurus
1135	72.5	6.1	243	2	Q4MBS9_BACCE	Q4MBS9 bacillus ce	1208	72.5	6.1	521	2	Q4QUL3_HAE18	Q4QUL3 haemophilus
1136	72.5	6.1	255	2	Q7M2C0_LEIMM	Q7M2C0 leishmania	1209	72.5	6.1	522	2	Q23444_CAEEL	Q23444 caenorhabdi
1137	72.5	6.1	267	2	Q4S673_TETNG	Q4S673 tetraodon n	1210	72.5	6.1	526	2	Q6PDF6_ACIAD	Q6PDF6 acinetobact
1138	72.5	6.1	269	2	Q4S673_TETNG	Q4S673 tetraodon n	1211	72.5	6.1	528	2	Q4RQ12_TETNG	Q4RQ12 tetraodon p
1139	72.5	6.1	269	2	Q8R8E9_FUSNN	Q8R8E9 fusobacteri	1212	72.5	6.1	539	2	Q5CUJ3_CRYPV	Q5CUJ3 cryospori
1140	72.5	6.1	278	2	Q516G0_MAGGR	Q516G0 magnaporthe	1213	72.5	6.1	539	2	Q7VSL1_BORPE	Q7VSL1 bordetella
1141	72.5	6.1	285	2	Q86DD6_CAEEL	Q86DD6 caenorhabdi	1214	72.5	6.1	539	2	Q7M446_BORPA	Q7M446 bordetella
1142	72.5	6.1	291	2	Q24561_MAIZE	Q24561 zea mays (m	1215	72.5	6.1	539	2	Q7WFK3_BORR	Q7WFK3 bordetella
1143	72.5	6.1	298	2	Q5WL74_BACSK	Q5WL74 bacillus cl	1216	72.5	6.1	562	2	Q5F1M1_MYTGA	Q5F1M1 mytilus gal
1144	72.5	6.1	298	2	Q8R2A8_MOUSE	Q8R2A8 mus musculu	1217	72.5	6.1	567	2	Q4YRZ9_PLABE	Q4YRZ9 plasmodium
1145	72.5	6.1	307	2	Q612V8_CAEBR	Q612V8 caenorhabdi	1218	72.5	6.1	574	2	Q6LH28_PHOPR	Q6LH28 photochacter
1146	72.5	6.1	308	2	Q6N472_RHOPA	Q6N472 rhodopseudo	1219	72.5	6.1	574	2	Q7USJ3_SYNFX	Q7USJ3 synchococc
1147	72.5	6.1	309	2	Q71UB1_BOVIN	Q71UB1 bos taurus	1220	72.5	6.1	614	2	Q21335_CAEEL	Q21335 caenorhabdi
1148	72.5	6.1	310	2	Q5J2F7_CHIHI	Q5J2F7 chimeritogal	1221	72.5	6.1	635	2	Q5SCD6_DICDI	Q5SCD6 dictyosteli
1149	72.5	6.1	310	2	Q5WL95_BACSK	Q5WL95 bacillus cl	1222	72.5	6.1	642	2	Q5SCD6_DICDI	Q5SCD6 dictyosteli
1150	72.5	6.1	315	2	Q5MPB4_9DIPF	Q5MPB4 dermatobia	1223	72.5	6.1	660	2	Q8AW53_BRARE	Q8AW53 brachyodan
1151	72.5	6.1	320	1	QXAA2_LACIA	QXAA2 lactococcus	1224	72.5	6.1	662	2	Q6G493_BAREE	Q6G493 bartonella
1152	72.5	6.1	325	2	Q9C119_LACIA	Q9C119 lactococcus	1225	72.5	6.1	664	2	Q5TYU4_BRARE	Q5TYU4 bartonella
1153	72.5	6.1	336	2	Q17077_CAEEL	Q17077 caenorhabdi	1226	72.5	6.1	666	1	KUP_STRA3	Q8575 streptococc
1154	72.5	6.1	348	2	Q833B9_ENTFA	Q833B9 enterococcu	1227	72.5	6.1	670	2	Q4IN97_GIBZE	Q4IN97 gibberella
1155	72.5	6.1	348	2	Q99924_9TELE	Q99924 cyprinella	1228	72.5	6.1	671	2	Q6MCRO_PARMU	Q6MCRO parachlamyd
1156	72.5	6.1	350	2	Q835L2_ENTFA	Q835L2 enterococcu	1229	72.5	6.1	688	2	Q8ERK6_SHEON	Q8ERK6 shewanella
1157	72.5	6.1	355	2	Q5UBS6_TECOL	Q5UBS6 escherichia	1230	72.5	6.1	696	2	Q9TU72_MUSVI	Q9TU72 muscista vis
1158	72.5	6.1	356	2	Q57A42_BRUBA	Q57A42 bruceella su	1231	72.5	6.1	704	2	Q5IWR2_9POAL	Q5IWR2 diptherium
1159	72.5	6.1	356	2	Q8FXM4_BRUBA	Q8FXM4 bruceella su	1232	72.5	6.1	717	2	Q7RICO_PLAYO	Q7RICO plasmodium
1160	72.5	6.1	360	2	Q70US3_DIRIM	Q70US3 dictyofilia	1233	72.5	6.1	718	2	Q48872_LACSK	Q48872 lactobacilli
1161	72.5	6.1	363	2	Q6GHU9_BACHK	Q6GHU9 bacillus th	1234	72.5	6.1	733	2	Q5EK43_LACSK	Q5EK43 lactobacilli
1162	72.5	6.1	365	2	Q4L629_STRAJ	Q4L629 staphylococ	1235	72.5	6.1	734	2	Q4JV05_CORYK	Q4JV05 corynebacte
1163	72.5	6.1	374	2	Q8MMR0_SHEEP	Q8MMR0 ovis aries	1236	72.5	6.1	756	2	Q6ZPE2_MOUSE	Q6ZPE2 mus musculu
1164	72.5	6.1	377	2	Q4R215_VABRI	Q4R215 vargula h11	1237	72.5	6.1	769	2	Q8C9E3_MOUSE	Q8C9E3 mus musculu
1165	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1238	72.5	6.1	789	2	Q9N3Y9_CAEEL	Q9N3Y9 caenorhabdi
1166	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1239	72.5	6.1	803	2	Q4LBR5_STABU	Q4LBR5 staphylococ
1167	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1240	72.5	6.1	832	2	Q5L7L5_BACPN	Q5L7L5 bacteroides
1168	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1241	72.5	6.1	832	2	Q64MT1_BACPN	Q64MT1 bacteroides
1169	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1242	72.5	6.1	848	2	Q8VZH3_ARATH	Q8VZH3 arabidopsis
1170	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1243	72.5	6.1	848	2	Q9S1U2_ARATH	Q9S1U2 arabidopsis
1171	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1244	72.5	6.1	858	2	Q741B5_LACIO	Q741B5 lactobacilli
1172	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1245	72.5	6.1	978	2	Q4UH31_THENM	Q4UH31 theileria a
1173	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1246	72.5	6.1	1103	2	Q753M8_ASHDO	Q753M8 ashbya goss
1174	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1247	72.5	6.1	1238	2	Q5CUC4_CRYPV	Q5CUC4 cryospori
1175	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1248	72.5	6.1	1291	2	Q7Q4O9_ANODA	Q7Q4O9 anopheles g
1176	72.5	6.1	379	1	Q9B371_CHIHI	Q9B371 chimeritogal	1249	72.5	6.1	1304	2	Q8NMU0_DICDI	Q8NMU0 dictyosteli
1177	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona th	1250	72.5	6.1	1340	2	Q51C25_ENTHI	Q51C25 entamoeba h
1178	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona th	1251	72.5	6.1	1357	2	Q817K7_CAEEL	Q817K7 caenorhabdi
1179	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona pa	1252	72.5	6.1	1461	2	Q55BC8_DICDI	Q55BC8 dictyosteli
1180	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona pa	1253	72.5	6.1	1472	2	Q4MMW3_ASPPU	Q4MMW3 aspergillus
1181	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1254	72.5	6.1	1526	2	Q19611_CAEEL	Q19611 caenorhabdi
1182	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1255	72.5	6.1	1689	2	Q8QZFA_VITRU	Q8QZFA vitru
1183	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1256	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1184	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1257	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1185	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1258	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1186	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1259	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1187	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1260	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1188	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1261	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1189	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1262	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1190	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1263	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1191	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1264	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1192	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1265	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1193	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1266	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1194	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1267	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1195	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1268	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1196	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1269	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1197	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1270	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1198	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1271	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru
1199	72.5	6.1	379	2	Q9G1C4_PLAGO	Q9G1C4 ochotona ca	1272	72.5	6.1	1689	2	Q991H9_VITRU	Q991H9 vitru

1273	72	6.0	227	2	Q7Y6X7_TIGCA	Q7Y6X7_tigriopus c	1346	72	6.0	468	2	Q94K50_ARATH	Q94K50_arabidopsis
1274	72	6.0	239	2	Q20S51_URSAM	Q20S51_ursus amerl	1347	72	6.0	479	1	CO06_YEAST	P5316_saccharomyc
1275	72	6.0	249	2	Q8E9R2_SHEON	Q8E9R2_sheenas amerl	1348	72	6.0	497	2	Q9FW59_ARATH	Q9FW59_arabidopsis
1276	72	6.0	254	2	Q812U8_BACCR	Q812U8_bacillus ce	1349	72	6.0	514	2	Q5TW51_ANOGA	Q5TW51_anopheles g
1277	72	6.0	254	2	Q81MK0_BACAN	Q81MK0_bacillus an	1350	72	6.0	518	2	Q7VQX6_CANBF	Q7VQX6_candidatus
1278	72	6.0	266	2	Q55BZ2_DICDI	Q55BZ2_dicystosell	1351	72	6.0	523	2	Q86YB4_HUMAN	Q86YB4_homo sapien
1279	72	6.0	276	2	Q9HJY7_THEAC	Q9HJY7_thermoplasma	1352	72	6.0	530	2	Q651Z2_ASF	Q651Z2_african swi
1280	72	6.0	279	2	Q9XXH1_CAEEL	Q9XXH1_caenorhabdi	1353	72	6.0	548	2	Q5CIG1_CRYHO	Q5CIG1_cryptospori
1281	72	6.0	286	2	Q6HKY7_BACHK	Q6HKY7_bacillus th	1354	72	6.0	552	2	Q6NMU7_CORDI	Q6NMU7_corynebacte
1282	72	6.0	290	2	Q6SHA6_BBACT	Q6SHA6_uncultured	1355	72	6.0	553	2	Q97SL9_SULFO	Q97SL9_sulfolobus
1283	72	6.0	299	2	Q4NM76_SMICC	Q4NM76_articobacte	1356	72	6.0	556	2	Q5SND9_CRYNE	Q5SND9_cryptococcu
1284	72	6.0	303	2	Q64RZ2_BACFR	Q64RZ2_bacteroides	1357	72	6.0	556	2	Q9JTN6_ARATH	Q9JTN6_arabidopsis
1285	72	6.0	306	2	Q6HWV3_CABR	Q6HWV3_bacillus an	1358	72	6.0	562	2	Q6CF79_YARLI	Q6CF79_yarrowia li
1286	72	6.0	306	2	Q8Y9B0_LISMO	Q8Y9B0_listeria mo	1359	72	6.0	584	2	Q5SUJ3_CRYNE	Q5SUJ3_cryptococcu
1287	72	6.0	306	2	Q60DA2_LEPOC	Q60DA2_leptostrept	1360	72	6.0	594	2	Q7L8X9_HUMAN	Q7L8X9_homo sapien
1288	72	6.0	311	2	Q61G56_CABER	Q61G56_caenorhabdi	1361	72	6.0	596	2	Q8R7C9_THERM	Q8R7C9_thermoanaer
1289	72	6.0	311	2	Q8VF62_MOUSE	Q8VF62_mus musculu	1362	72	6.0	599	2	Q5SUJ0_CRYNE	Q5SUJ0_cryptococcu
1290	72	6.0	315	2	Q5HSN1_CAMOR	Q5HSN1_campylobact	1363	72	6.0	600	2	Q42972_SCHPO	Q42972_schistosach
1291	72	6.0	317	2	Q9CKI6_PASNU	Q9CKI6_pasteurella	1364	72	6.0	601	2	Q5KHV7_CRYNE	Q5KHV7_cryptococcu
1292	72	6.0	320	2	Q7ZUC3_BARE	Q7ZUC3_brachydanio	1365	72	6.0	610	2	Q84ZX2_GCHLO	Q84ZX2_tetraselmis
1293	72	6.0	324	2	Q88TJ9_LACPL	Q88TJ9_lactobacill	1366	72	6.0	615	2	Q54ZB7_DICDI	Q54ZB7_dicystosell
1294	72	6.0	334	2	Q88XJ9_LACPL	Q88XJ9_lactobacill	1367	72	6.0	619	2	Q4WY73_ASPRU	Q4WY73_aspergillus
1295	72	6.0	335	2	Q9ZYJ2_ORYAF	Q9ZYJ2_oryzoeurop	1368	72	6.0	630	2	Q24608_DITAC	Q24608_diatomus ca
1296	72	6.0	338	2	Q9XTR2_CAEEL	Q9XTR2_caenorhabdi	1369	72	6.0	643	2	Q565Z5_YBACT	Q565Z5_uncultured
1297	72	6.0	339	2	Q97GD6_CLOAB	Q97GD6_clostridium	1370	72	6.0	673	2	Q61DB7_CABER	Q61DB7_caenorhabdi
1298	72	6.0	343	2	Q9TD07_9SMEG	Q9TD07_rachovia ma	1371	72	6.0	692	2	Q6DD44_XENLA	Q6DD44_xenopus lae
1299	72	6.0	343	2	Q9B4H5_UMASC	Q9B4H5_uma scopari	1372	72	6.0	696	2	Q957J9_HUMAN	Q957J9_homo sapien
1300	72	6.0	343	2	Q8SAT6_UMASC	Q8SAT6_uma scopari	1373	72	6.0	696	2	Q9UBH6_HUMAN	Q9UBH6_homo sapien
1301	72	6.0	354	2	Q4VTY7_SHIBO	Q4VTY7_shigella bo	1374	72	6.0	712	2	Q94EK6_PEA	Q94EK6_pisum sativ
1302	72	6.0	356	2	Q61CY6_CABER	Q61CY6_caenorhabdi	1375	72	6.0	716	2	Q7N7J2_PHOLL	Q7N7J2_photornabdu
1303	72	6.0	363	2	Q52R87_LEPOC	Q52R87_leptostreus	1376	72	6.0	721	2	Q67YLA6_SYWTH	Q67YLA6_symbiobacte
1304	72	6.0	364	2	Q7YMW5_CAEEL	Q7YMW5_caenorhabdi	1377	72	6.0	736	2	Q7YU76_DROME	Q7YU76_drosophila
1305	72	6.0	368	2	Q4KM24_9G0B1	Q4KM24_kribia nana	1378	72	6.0	768	2	Q50PC7_ENTHI	Q50PC7_entamoeba h
1306	72	6.0	379	1	CYB_GEOB1	Q6ZS5_geomyia pine	1379	72	6.0	772	2	Q75JP4_DICDI	Q75JP4_dicystosell
1307	72	6.0	379	1	CYB_THOVA	Q6ZS5_geomyia pine	1380	72	6.0	788	2	Q8TD05_HUMAN	Q8TD05_homo sapien
1308	72	6.0	379	2	Q9THD6_ORYAF	Q9THD6_oryzoeurop	1381	72	6.0	796	2	Q75DE7_ASHGO	Q75DE7_ashbya gos
1309	72	6.0	379	2	Q4VWH4_TUPGL	Q4VWH4_tupala glis	1382	72	6.0	844	2	Q750H3_ASHGO	Q750H3_ashbya gos
1310	72	6.0	379	2	Q8MDV3_CRAGY	Q8MDV3_cratogeomys	1383	72	6.0	878	2	Q9VSK2_DROME	Q9VSK2_drosophila
1311	72	6.0	379	2	Q8W8K4_CRAGY	Q8W8K4_cratogeomys	1384	72	6.0	917	2	Q4HTB1_CAMUP	Q4HTB1_campylobact
1312	72	6.0	379	2	Q7TIO9_CRATY	Q7TIO9_cratogeomys	1385	72	6.0	928	2	Q660E1_BORCA	Q660E1_borrelia ga
1313	72	6.0	379	2	Q69803_CRAFU	Q69803_cratogeomys	1386	72	6.0	946	2	Q5B4J0_XENLA	Q5B4J0_xenopus lae
1314	72	6.0	379	2	Q5YJ77_9RODE	Q5YJ77_geomyia pers	1387	72	6.0	980	2	Q50VMS_ENTHI	Q50VMS_entamoeba h
1315	72	6.0	379	2	Q5YJ76_9RODE	Q5YJ76_geomyia pers	1388	72	6.0	1025	2	Q4Q398_LEIMA	Q4Q398_leishmania
1316	72	6.0	379	2	Q5YJ69_9RODE	Q5YJ69_geomyia pers	1389	72	6.0	1035	2	Q875W8_SACCA	Q875W8_saccharomyc
1317	72	6.0	379	2	Q5YJ66_9RODE	Q5YJ66_geomyia pine	1390	72	6.0	1038	1	YKD3_YEAST	P56097_saccharomyc
1318	72	6.0	379	2	Q5YJ65_9RODE	Q5YJ65_geomyia pine	1391	72	6.0	1094	1	DP0D_PLAFA	P30315_plasmodium
1319	72	6.0	386	1	CYB_SARGL	Q53848_sarcophyton	1392	72	6.0	1094	2	Q7K0I4_PLAF7	Q7K0I4_plasmodium
1320	72	6.0	391	2	Q8RLY7_SALET	Q8RLY7_salmonella	1393	72	6.0	1113	2	Q9XXK4_CAEEL	Q9XXK4_caenorhabdi
1321	72	6.0	391	2	Q8RLY9_SALET	Q8RLY9_salmonella	1394	72	6.0	1129	2	Q4ODH8_LEIMA	Q4ODH8_leishmania
1322	72	6.0	392	2	Q9LCN9_MICEC	Q9LCN9_microthomosp	1395	72	6.0	1220	1	PTC1_BRARE	PTC1_bryophyllum
1323	72	6.0	396	1	CYB_LAMFL	Q91C00_lampetra fl	1396	72	6.0	1275	1	TRP_DROME	P19334_drosophila
1324	72	6.0	396	1	Q4LW03_9BURK	Q4LW03_burkholderi	1397	72	6.0	1275	2	Q9VBE1_DROME	Q9VBE1_drosophila
1325	72	6.0	415	1	L52_ADBO2	P03262_human adeno	1398	72	6.0	1282	2	Q24809_ENTHI	Q24809_entamoeba h
1326	72	6.0	415	1	L52_ADBO5	P04396_human adeno	1399	72	6.0	1469	2	Q4WB59_ASPFU	Q4WB59_aspergillus
1327	72	6.0	415	2	Q6VGV2_9ADEN	Q6VGV2_human adeno	1400	72	6.0	1477	2	Q9C250_NEUPR	Q9C250_neurospora
1328	72	6.0	415	2	Q71BX5_ADE01	Q71BX5_human adeno	1401	72	6.0	1481	2	Q4NIM9_THERP	Q4NIM9_thelateria p
1329	72	6.0	418	2	Q9NTI9_HUMAN	Q9NTI9_homo sapien	1402	72	6.0	1513	2	Q7RVU0_NEUCR	Q7RVU0_neurospora
1330	72	6.0	418	2	Q6QFBS_LEGPN	Q6QFBS_legionella	1403	72	6.0	1566	2	Q4Z597_PLABE	Q4Z597_plasmodium
1331	72	6.0	418	2	Q6QFCS_LEGPN	Q6QFCS_legionella	1404	72	6.0	2387	2	Q5CYF5_CRYPV	Q5CYF5_cryptospori
1332	72	6.0	419	2	Q661Y4_XENTR	Q661Y4_xenopus tro	1405	72	6.0	3010	2	Q9QIX1_SHEPC	Q9QIX1_hepatitis c
1333	72	6.0	444	2	Q6GKS5_STEAR	Q6GKS5_staphylococ	1406	72	6.0	3010	2	Q9QIX2_SHEPC	Q9QIX2_hepatitis c
1334	72	6.0	444	2	Q5HUX5_STAAC	Q5HUX5_staphylococ	1407	72	6.0	84	2	Q5JH15_PYROK	Q5JH15_pyrococcus
1335	72	6.0	448	1	INVX_SGHP	Q42878_echinosacch	1408	72	6.0	161	2	Q48242_9NEOP	Q48242_dennysus som
1336	72	6.0	448	2	Q460J4_DROME	Q460J4_drosophila	1409	72	6.0	198	2	Q86X19_HUMAN	Q86X19_homo sapien
1337	72	6.0	453	2	Q7NWT7_CHRVO	Q7NWT7_chromobacte	1410	72	6.0	200	2	Q5UON8_TUMTV	Q5UON8_tumtvirus
1338	72	6.0	453	2	Q7ABD9_STANV	Q7ABD9_staphylococ	1411	72	6.0	206	2	Q8YEB1_LEPIN	Q8YEB1_leptocoptia
1339	72	6.0	453	2	Q99XF2_STAMM	Q99XF2_staphylococ	1412	72	6.0	210	2	Q376B2_TRYBO	Q376B2_trypanosplas
1340	72	6.0	456	2	Q59NM0_CANAL	Q59NM0_candida alb	1413	72	6.0	225	1	VME1_IBV6	P51362_avian infec
1341	72	6.0	462	2	Q4KOH6_STRPN	Q4KOH6_streptococc	1414	72	6.0	227	2	Q9GAT7_OCHCO	Q9GAT7_ochococna co
1342	72	6.0	464	2	Q61HJ0_CABER	Q61HJ0_caenorhabdi	1415	72	6.0	229	2	Q7NBZ9_MYCGA	Q7NBZ9_mycoplasma
1343	72	6.0	465	2	Q9RDT2_STAAL	Q9RDT2_staphylococ	1416	72	6.0	235	2	Q03191_9HVMR	Q03191_mononoriur
1344	72	6.0	467	2	Q57V83_STRYP	Q57V83_trypanosoma	1417	72	6.0	237	2	Q7TW45_MYCBO	Q7TW45_mycobacteri
1345	72	6.0	467	2	Q57V84_STRYP	Q57V84_trypanosoma	1418	72	6.0	237	2	Q06Z51_MYCTU	Q06Z51_mycobacteri



1419	71.5	6.0	246	08YB21_BRUME	08YB21 bruceella me
1420	71.5	6.0	254	08LX09_BPHAE	08LX09 lamnaria d
1421	71.5	6.0	255	066460_EAV	066460 equine arte
1422	71.5	6.0	257	071W44_LISMF	071W44 listeria mo
1423	71.5	6.0	266	08XP47_CIOPE	08XP47 clostridium
1424	71.5	6.0	266	051P55_PERAP	051P55 perognathus
1425	71.5	6.0	266	051P53_PERPA	051P53 perognathus
1426	71.5	6.0	270	08H1Y5_ERLO	08H1Y5 perognathus
1427	71.5	6.0	301	09C074_LACLA	09C074 lactococcus
1428	71.5	6.0	314	OR39_MOUSE	OR39 mouse
1429	71.5	6.0	320	09FAT0_VIBPA	09FAT0 vibrio para
1430	71.5	6.0	326	071853_HUMAN	071853 homo sapien
1431	71.5	6.0	326	09BFA5_CERAT	09BFA5 ceratotheri
1432	71.5	6.0	326	09BFS7_HYLCO	09BFS7 hylobates c
1433	71.5	6.0	328	089R48_BRAUA	089R48 bradyrhizob
1434	71.5	6.0	332	08GIP3_THENE	08GIP3 thermotoga
1435	71.5	6.0	334	09T200_CAEEL	09T200 caenorhabdi
1436	71.5	6.0	336	09THE4_SORRA	09THE4 sorex radde
1437	71.5	6.0	336	079425_MEORO	079425 neomys fodi
1438	71.5	6.0	336	0800E8_TETNG	0800E8 tetradodon n
1439	71.5	6.0	338	0800G2_TETNG	0800G2 tetradodon n
1440	71.5	6.0	339	04UMM1_RICPE	04UMM1 rickettsia
1441	71.5	6.0	339	08RD25_THETN	08RD25 thermocaeer
1442	71.5	6.0	341	098R21_GUITH	098R21 yellardiaria
1443	71.5	6.0	342	05ND81_YERAL	05ND81 yersinia al
1444	71.5	6.0	342	VG74_HHV8	VG74 human herpe
1445	71.5	6.0	342	090387_HHV8	090387 human herpe
1446	71.5	6.0	342	077Q35_HHV8	077Q35 human herpe
1447	71.5	6.0	348	RMFD_VIBCH	RMFD vibrio chol
1448	71.5	6.0	348	099972_9TELE	099972 vibrioinella
1449	71.5	6.0	350	05QMM0_IDILO	05QMM0 idiomarina
1450	71.5	6.0	355	08YDX2_BRUME	08YDX2 bruceella me
1451	71.5	6.0	360	08H1B6_9SCIU	08H1B6 callosclutru
1452	71.5	6.0	362	065CY4_BACLD	065CY4 bacillus ii
1453	71.5	6.0	362	06DFP2_MOUSE	06DFP2 mus musculu
1454	71.5	6.0	366	MRRIA_SHEEP	MRRIA ovis aries
1455	71.5	6.0	369	070VP8_SORMI	070VP8 sorex minut
1456	71.5	6.0	375	06RKFP_9GAMA	06RKFP human herpe
1457	71.5	6.0	377	04R215_VARRI	04R215 vargula hii
1458	71.5	6.0	379	CYB_OCHCO	095315 ochotona co
1459	71.5	6.0	379	CYB_OCHFO	094955 ochotona fo
1460	71.5	6.0	379	CYB_SORRA	079462 sorex radde
1461	71.5	6.0	379	CYB_SPERA	09FF55 spermophilu
1462	71.5	6.0	379	048007_PPRAP	048007 perognathus
1463	71.5	6.0	379	08MEK3_THOTA	08MEK3 thiomys ta
1464	71.5	6.0	379	0952R3_GLASA	0952R3 glaucomyx s
1465	71.5	6.0	379	09TF66_SPESP	09TF66 spermophilu
1466	71.5	6.0	379	034661_GLASA	034661 glaucomyx s
1467	71.5	6.0	379	071BW1_GLASA	071BW1 glaucomyx s
1468	71.5	6.0	379	0698Q0_CRAFU	0698Q0 cratogeomys
1469	71.5	6.0	379	0508P4_9RODE	0508P4 liomys pict
1470	71.5	6.0	379	0508M2_9RODE	0508M2 dipodomys d
1471	71.5	6.0	379	0508K6_9RODE	0508K6 chactodipus
1472	71.5	6.0	381	08ZXP7_PYPAR	08ZXP7 pyrobaculum
1473	71.5	6.0	381	06RKFP_9GAMA	06RKFP human herpe
1474	71.5	6.0	381	079571_9CHON	079571 mustelus ma
1475	71.5	6.0	382	09NYN8_HUMAN	09NYN8 homo sapien
1476	71.5	6.0	383	YIY4_SCHPO	YIY4 schizosacch
1477	71.5	6.0	386	0XYR_PIG	0XYR sus scrofa
1478	71.5	6.0	386	08RB76_THETN	08RB76 thermomane
1479	71.5	6.0	388	08SQ91_NYCTH	08SQ91 nycteris th
1480	71.5	6.0	388	08SQ93_9CHIR	08SQ93 nycteris gr
1481	71.5	6.0	390	ITR_CATCO	090334 catostomus
1482	71.5	6.0	392	09AH88_STRPN	09AH88 streptococc
1483	71.5	6.0	396	05NIP0_PPRAT	05NIP0 pericissella
1484	71.5	6.0	404	04UN16_RICPE	04UN16 rickettsia
1485	71.5	6.0	407	06DG01_BRARE	06DG01 brachydiano
1486	71.5	6.0	410	08ZAH6_STRAM	08ZAH6 streptomyce
1487	71.5	6.0	418	07NKE2_GLOVI	07NKE2 gloeobacter
1488	71.5	6.0	419	07V4C4_PROMM	07V4C4 prochloroco
1489	71.5	6.0	424	04K127_STRPN	04K127 streptococc
1490	71.5	6.0	424	04K148_STRPN	04K148 streptococc
1491	71.5	6.0	431	066H32_RAT	066H32 rattus norv

1492	71.5	6.0	435	071XN9_LISMF	071XN9 listeria mo
1493	71.5	6.0	435	089117_BRAJA	089117 bradyrhizob
1494	71.5	6.0	435	08YSE0_LISMO	08YSE0 listeria in
1495	71.5	6.0	435	0929P5_LISIN	0929P5 listeria in
1496	71.5	6.0	442	0625Z7_CABER	0625Z7 caenorhabdi
1497	71.5	6.0	453	0551B0_CRYNE	0551B0 cryptococcu
1498	71.5	6.0	453	05KMA2_CRYNE	05KMA2 cryptococcu
1499	71.5	6.0	464	059Q41_CANAL	059Q41 candida alb
1500	71.5	6.0	466	05A268_EMENI	05A268 aspergillus
ALIGNMENTS					
RESULT 1					
MENTO_HUMAN					
ID	MENTO_HUMAN	STANDARD;	PRT;	234 AA.	
AC	095772;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	13-SEP-2005 (Rel. 48, Last annotation update)				
DE	MLN64 N-terminal domain homolog (STRAD3 N-terminal-like protein).				
GN	Name=STRAD3ML; Synonyms=MENTHO; ORFNames=UNQ855/PRO1864;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RP	NUCLEOTIDE SEQUENCE, CHARACTERIZATION, TOPOLOGY, PHOSPHORYLATION, AND				
RP	ALTERATIVE INITIATION.				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=22384343; PubMed=12393907; DOI=10.1074/jbc.M208290200;				
RT	Alpy F., Wendling C., Rio M.-C., Tomasello C.;				
RT	"MENTHO, a MLN64 homologue devoid of the START domain.";				
RT	J. Biol. Chem. 277:50780-50787(2002).				
RL	[2]				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].				
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;				
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,				
RA	Bacon J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,				
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,				
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,				
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vages A.,				
RA	Yandura R.L., Wetanabe C., Weand D., Woods K., Xie M.-H.,				
RA	Yandura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,				
RA	Wood M.I., Godowski P.J., Gray A.M.;				
RT	"The secreted protein discovery initiative (SPDI), a large-scale				
RT	effort to identify novel human secreted and transmembrane proteins: a				
RT	bioinformatics assessment.";				
RL	Genome Res. 13:2265-2270(2003).				
RL	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Arnett C., Wohldmann P., Le T.;				
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.				
RL	[4]				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].				
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Ditchevko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Ueda T.B., Tohiyuki S., Carninci P., Prange C.,				
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.U., McKernan K.J., Malek U.A., Gunnaracne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huiyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				



OC Mammalia; Eutheria; Earchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muroidae; Muridae; Murinae; Mus.  
 OC NCBI\_Taxid=10090;  
 [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 2).  
 RC SRR141-65781/657; TISSUE=Cerebellum; and Kidney;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kaubawa T., Adachi J., Bono H., Kondo S.,  
 RA Nakado I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schobach C., Gotohori T.,  
 RA Baldrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,  
 RA Della E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough U.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglocz D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pettes G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Zimin P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shirekhi T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Heien F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueding T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Bullyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska J., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal  
 membrane protein (by similarity).  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC -1- Event=Alternative splicing; Named isoforms=2;  
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RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bernaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carrincci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RA Strausberg R.,  
RL EMBL: BC075752; AAH75752.1; -, mRNA.  
DR ZFIN: ZDB-GENE-040718-4; ZGC:86628.  
SQ SEQUENCE 227 AA; 25485 MW; 24C6AD8FFA985C6 CRC64;  
Query Match 66.6%; Score 796; DB 2; Length 227;  
Best Local Similarity 68.3%; Pred. No. 2,4e-64;  
Matches 155; Conservative 31; Mismatches 39; Indels 2; Gaps 2;  
QY 8 MENALTGSSGSHSLRNHINSINPTQLMARIESYEGREKGISDVRRTECLFPTDLFVT 67  
DB 1 MDSQSSSVGSRRANLGGIGINSTPIISARVESYAGEKKGISDVRRTECLFPTDLFVT 60  
QY 68 LMTIETLNNGGIENTLEKEVMQDYSSYEDIFILAVFPFKVLLAAYCRHMMWYA 127  
DB 61 LMTIETLNNGGIIQOQLEQELVKYDKHKSFPDFILVFRPAALITLVAACKLHMMWYA 120  
QY 128 LTTAVTSAPFLAKVILSKLFSQAGFYVLPILISFILAMITWFLDFKVLPOEAEENRLL 187  
DB 121 ITRAITTGFIIVKVVVSKLSQAGFYVLPILISFILAMITWFLDFKVLPOEAGDEIRYL 180  
QY 188 IVQDASERALLI-PGSLSDGQFYSPPESEAGS-EBAEEKODSEKPL 222  
DB 181 SVQNRLEHREPLPGPLSEGLFYSPPESLADSDDEDLDKDLKRPV 227  
RESULT 5  
Q6DFR7\_XENTR PRELIMINARY; PRT; 448 AA.  
AC O6DFR7;  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE START domain containing 3.  
GN Name=stard3-prov;  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodidae; Xenopus; Silurana.  
NCBI\_TaxID=8364;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carrincci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RA Klein S., Gerhard D.S.,  
RL EMBL: BC076666; AAH76666.1; -, mRNA.  
DR SMR: Q6DFR7; 236-443.  
DR GO: GO:0005739; C:mitochondrion; IEA.  
DR GO: GO:0015485; F:cholesterol binding; IEA.  
DR GO: GO:0017127; F:cholesterol transporter activity; IEA.  
DR GO: GO:0008289; F:lipid binding; IEA.  
DR GO: GO:0008693; P:lipid transport; IEA.  
DR GO: GO:000694; P:steroid biosynthesis; IEA.  
DR InterPro: IPR000799; STAR.  
DR InterPro: IPR002913; START.  
DR Pfam: PF01852; START; 1.  
DR PRINTS: PR00978; STARPROTEIN.  
DR SMART: SM00234; START; 1.  
DR PROSITE: PS50848; START; 1.  
SQ SEQUENCE 448 AA; 50926 MW; 2686D07C737D4204 CRC64;  
Query Match 58.6%; Score 700.5; DB 2; Length 448;  
Best Local Similarity 61.1%; Pred. No. 2.8e-55;  
Matches 143; Conservative 29; Mismatches 49; Indels 13; Gaps 4;  
QY 1 MNHLP-EDMENALTGSSGSHSLRNHINSINPTQLMARIESYEGREKKGISDVRRTECL 56  
DB 1 MTKLPDGFQFDLRLSPALINSINSQNHVFSPHSLPRLP-----EORRVISDVRRTECL 54  
QY 57 LFTVFDLPTLTLMTIETLNNGGIENTLEKEVMQDYSSYEDIFILAVRFPVLLAAYA 116  
DB 55 LFTVFDLPTLTLMTIETLNNGGIENTLEKEVMQDYSSYEDIFILAVRFPVLLAAYA 114  
QY 117 VCRLRHMMWALATLTAATSAPFLAKVILSKLFSQAGFYVLPILISFILAMITWFLDFKVL 176  
DB 115 IVRLRHMMWALAITTVTSAPFLAKVILSKLFSQAGFYVLPILISFILAMITWFLDFKVL 174  
QY 177 POEAEENRLLIVQDASERALLI-PGSLSDGQFYSPPESEAGSEBAEEKODSEK 229  
DB 175 TQEAEEERWYMAVQAAGSHHPPLLYNGALSDGQFYSPPESEAGSD--NEFDDEE 226  
RESULT 6  
Q6PF40\_XENLA PRELIMINARY; PRT; 444 AA.  
AC O6PF40;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE MGC68989 protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodidae; Xenopus; Xenopus.  
NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spine;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.,  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RX Klein S., Strausberg R.,  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC057738; AAH57738.1; -; mRNA.  
DR SMR; Q6PF40; 232-439.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
DR GO; GO:0015485; F:cholesterol binding; IEA.  
DR GO; GO:0017127; F:cholesterol transporter activity; IEA.  
DR GO; GO:0006829; F:lipid binding; IEA.  
DR GO; GO:0006869; F:lipid transport; IEA.  
DR GO; GO:0006694; P:steroid biosynthesis; IEA.  
DR InterPro; IPR000799; SCAR.  
DR InterPro; IPR002913; START.  
DR Pfam; PF01852; START; 1.  
DR PRINTS; PR00978; STARPROTEIN.  
DR SMART; SM00234; START; 1.  
DR PROSITE; PS50848; START; 1.  
SQ SEQUENCE 444 AA; 50572 MW; 7BEA97317BF48358 CRC64;  
Query Match 58.5%; Score 698.5; DB 2; Length 444;  
Best Local Similarity 60.9%; Pred. No. 4.2e-55;  
Matches 140; Conservative 30; Mismatches 51; Indels 9; Gaps 3;  
QY 1 MNHLPEDEMNALTSQSSHASLRNHSINPTOLMARIESYEGREKKGISDVRRFTFC 60  
DB 1 MTKLPGEFQDPLESLPALASMSQSHVSPSLPR-----EQRRASDVRRFTFC 54  
QY 61 FDLIFVTLILWIIELNVNGGIENTLEKEVMQDYSSYDIFLLAVFRKVIILAYAVRL 120  
DB 55 FDLIFISLILWIIELNVNGGIENTLEKEVMQDYSSYDIFLLAVFRKVIILAYAVRL 114  
QY 121 RHMWAIALTTVAATVSLAKYILSLFSGAGFYVLPISPIFLAMIEWPFDPKVLPOEA 180  
DB 115 RHMWAIALTTVAATVSLAKYILSLFSGAGFYVLPISPIFLAMIEWPFDPKVLPOEA 174  
QY 181 EENENLLIVODASERAAI-PEGISDGOFYSPPESEASEEAEKQSDSEK 229  
DB 175 EENENLLIVODASERAAI-PEGISDGOFYSPPESEASEEAEKQSDSEK 222  
RESULT 7  
OGCNT3 XENLA PRELIMINARY; PRT; 448 AA.  
ID OG CNT3-  
AC OG CNT3-  
DT 05-JUL-2004 (Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, last sequence update)  
DE 05-JUL-2004 (Tremblrel. 27, last annotation update)  
DT MCC80895 protein.  
GN Name=MCC80895;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodidae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Maira M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.,  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX Klein S., Gerhardt D.S.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073419; AAH73419.1; -; mRNA.  
DR SMR; O6GNT3; 235-443.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
DR GO; GO:0015485; F:cholesterol binding; IEA.  
DR GO; GO:0017127; F:cholesterol transporter activity; IEA.  
DR GO; GO:0006829; F:lipid binding; IEA.  
DR GO; GO:0006869; F:lipid transport; IEA.  
DR GO; GO:0006694; P:steroid biosynthesis; IEA.  
DR InterPro; IPR000799; SCAR.  
DR InterPro; IPR002913; START.  
DR Pfam; PF01852; START; 1.  
DR PRINTS; PR00978; STARPROTEIN.  
DR SMART; SM00234; START; 1.  
DR PROSITE; PS50848; START; 1.  
SQ SEQUENCE 448 AA; 51279 MW; 472FF8E7C3B2F5E4 CRC64;  
Query Match 57.2%; Score 684; DB 2; Length 448;  
Best Local Similarity 59.7%; Pred. No. 9e-54;  
Matches 139; Conservative 34; Mismatches 48; Indels 12; Gaps 4;  
QY 1 MNHLPEDEMNALTSQSSHASLRNHSINPTOLMARIESYEGREKKGISDVRRFTFC 56  
DB 1 MTKLPGEFQDPLESLPALASMSQSHVSPSLPR-----EQRRASDVRRFTFC 54  
QY 57 LFTVFDLLFVTLILWIIELNVNGGIENTLEKEVMQDYSSYDIFLLAVFRKVIILAYA 116

DB 55 LEVTFDLFIISLMIETNTNGIEKNLEBEIILHYDFKNSFPDIYLLAVRPSVLIIA 114  
 QY 117 VCRIRHMMALITLTATYSAFLAKVLISKFSGAGFQYVPIISFLIAMIETPLDKVL 176  
 DB 115 IYALRHMMALITLTATYSAFLIVIOSGLLSKGAFTYVPIVFSVLAMLETFDLKVL 174  
 QY 177 POAEERENLLIYO-DASERAAVLPGLSDGFSPSPSEBAGE-EAEEKQDS 227  
 DB 175 TQAEERERWYTAQAAPANHPPIYNGTLSDGFSPSPSEBAGEDEDEEA 227

RESULT 8  
 MLN64\_HUMAN  
 ID MLN64\_HUMAN STANDARD; PRT; 445 AA.  
 AC Q14845; Q96HM9;  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE MLN 64 protein (StAR-related lipid transfer protein 3) (STARD3) (STARD domain-containing protein 3) (CAB1 protein).  
 GN Name=STARD3; Synonyms=CAB1, MLN64;  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Mammary carcinoma;  
 RX MEDLINE=96039245; PubMed=7490069;  
 RA Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,  
 RA Chénard M.-P., Lidereau R., Bassat P., Rio M.-C.;  
 RT "Identification of four novel human genes amplified and overexpressed in breast carcinoma and localized to the q11-q21.3 region of chromosome 17.";  
 RT Chromosome 17.;  
 RL Genomics 28:367-376(1995).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Oesophageal carcinoma;  
 RX MEDLINE=97413641; PubMed=9270027;  
 RA Hirayama N., Sasaki H., Ishizuka T., Kishi T., Sakamoto H., Onda M.,  
 RA Kishi H., Yazaki Y., Sugimura T., Terada M.;  
 RT "Isolation of a candidate gene, CAB1, for cholesterol transport to mitochondria from the c-ERBB-2 amplicon by a modified cDNA selection method.";  
 RT Cancer Res. 57:3548-3553(1997).  
 RL [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Lung, Skin, and Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang G.M., Hong L.,  
 RA Stachenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange S.J.,  
 RA Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Wooley K.C., Hale S., Garcia A.M., Gay L.U., Hultk S.W.,  
 RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Keeton M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska J., Smalins D.E.,  
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 216-445.  
 RX MEDLINE=20264523; PubMed=10802740; DOI=10.1038/75192;

RA Teuhshtla Y., Hurley J.H.;  
 RT "Structure and lipid transport mechanism of a StAR-related domain.";  
 RL Nat. Struct. Biol. 7:408-414(2000).  
 RN [5]  
 RP TOPOLOGY.  
 RX MEDLINE=21264925; PubMed=11053434; DOI=10.1074/jbc.M006279200;  
 RA Alpy F., Stoeckel M.-E., Dierich A., Beccha J.-M., Wendling C.,  
 RA Chénard M.-P., Vanter M.T., Gruenberg J., Tomasetto C., Rio M.-C.;  
 RT "The steroidogenic acute regulatory protein homolog MLN64, a late endosomal cholesterol-binding protein.";  
 RL J. Biol. Chem. 276:4261-4269(2001).  
 CC -1- FUNCTION: Binds and transports cholesterol. Promotes steroidogenesis in placenta and brain.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal membrane protein.  
 CC -1- SIMILARITY: Contains 1 MENTAL domain.  
 CC -1- DATABASE: NMB=Atlas Genet. Cytogenet. Oncol. Haematol.;  
 CC WWW=http://www.infobiochem.fr/services/chromocancer/Genes/MLN64ID202.html".  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 CC -----  
 DR EMBL: X80198; CA56489.1; -; mRNA.  
 DR EMBL: D38255; BAA22525.1; -; mRNA.  
 DR EMBL: BC008356; AAH08356.1; -; mRNA.  
 DR EMBL: BC008747; AAH08747.1; -; mRNA.  
 DR EMBL: BC025679; AAH25679.1; -; mRNA.  
 DR PIR: I38027; I38027.  
 DR PDB: 1EM2; X-ray; A=216-444.  
 DR Ensembl: ENSG00000131748; Homo sapiens.  
 DR HGNC: HGNC:17579; STARD3.  
 DR H-InvDB: HIX0013780; -.  
 DR MIM: 607048; -.  
 DR GO: GO:0005737; C:cytoplasm; TAS.  
 DR GO: GO:0008203; P:cholesterol metabolism; TAS.  
 DR GO: GO:0006629; P:lipid metabolism; TAS.  
 DR GO: GO:0006839; P:mitochondrial transport; TAS.  
 DR GO: GO:0008202; P:steroid metabolism; TAS.  
 DR InterPro: IPR000799; STAR.  
 DR InterPro: IPR002913; STAR\_lipid\_bd.  
 DR Pfam: PF01852; STAR\_1.  
 DR PRINTS: PR00978; STARP/PROTEIN.  
 DR SMART: SM00234; STAR\_1.  
 DR PROSITE: PS50846; STAR\_1.  
 DR 3D-structure: Lipid transport; Lipid-binding; Steroidogenesis; Transmembrane; Transport.  
 KW TOPO DOM 1 51  
 FT TOPO DOM 51 72  
 FT TRANSMEM 72 72  
 FT TOPO DOM 72 94  
 FT TRANSMEM 94 115  
 FT TOPO DOM 115 120  
 FT TRANSMEM 120 141  
 FT TOPO DOM 141 141  
 FT TOPO DOM 141 148  
 FT TRANSMEM 148 149  
 FT TOPO DOM 149 170  
 FT TOPO DOM 170 445  
 FT TOPO DOM 445 445  
 FT DOMAIN 445 445  
 FT DOMAIN 445 443  
 FT DOMAIN 443 443  
 FT CONFLICT 117 117  
 FT CONFLICT 117 116  
 FT CONFLICT 116 216  
 FT HELIX 233 253  
 FT HELIX 253 253  
 FT HELIX 253 255  
 FT HELIX 255 258  
 FT HELIX 258 264  
 FT STRAND 264 264  
 FT STRAND 264 267  
 FT STRAND 267 276  
 FT STRAND 276 277  
 FT STRAND 277 279  
 FT STRAND 279 280  
 FT HELIX 280 299  
 FT HELIX 299 299  
 FT TURN 302 302  
 G -> R (in Ref. 3; AAH08356/AAH25679).  
 G -> A (in Ref. 3; AAH25679).



FT	HELIX	304	307
FT	TURB	308	310
FT	TURB	312	313
FT	TURB	314	323
FT	TURB	324	326
FT	TURB	327	334
FT	TURB	337	337
FT	TURB	338	341
FT	TURB	342	342
FT	TURB	345	355
FT	TURB	359	366
FT	TURB	370	371
FT	TURB	376	377
FT	TURB	379	380
FT	TURB	382	383
FT	TURB	386	392
FT	TURB	397	398
FT	TURB	400	406
FT	TURB	408	409
FT	HELIX	416	440
FT	TURB	441	442
SQ	SEQUENCE	445 AA;	50474 MW; 62BED5C3EDA0DEF CRC64;
Query Match		55.6%;	Score 664; DB 1; Length 445;
Best Local Similarity		56.2%;	Pred. No. 66-52;
Matches 135;	Conservative	38;	Mismatches 45; Indels 22; Gaps 5;
OY	1 MNHLP----	EDMENAL-----	TGSGSSHASLRNHSINPTOLMARIESYEGREKKGISDV 51
Db	1 MSKLPRETRRLBRS	LPAVASTGSSLSHSQSSLSHLPPE-----	KRRASDV 49
OY	52 RRTCLFPTFPDL	LYTTLMTIELNVNGIENTLEKEVNOYDYSYFPIFLAVRFKVL 111	
Db	50 RRTCLFPTFPDL	FLISLMIETLNTGIRKNLEBOEIIOYNFKTSFPIFLAVRFKVL 109	
OY	112 ILAAVCGRLRMWMA	LTAVTSAPFLAKVILSKLFSGARGVLPPIISFLAMTETFL 171	
Db	110 LLGVAVALDRHMWVA	VTTLVSSAPFLIVKVLSELSSGARGVLPPIISFLAMTETFL 169	
OY	172 DFKVLPQAEERENR	LIVODASERALL-PGGLSDGQFVSPPESEAGSE-EAEEKODESK 229	
Db	170 DFKVLPQAEERENR	LIVODASERALL-PGGLSDGQFVSPPESEAGSE-EAEEKODESK 229	
RESULT 9			
OS3Y53 HUMAN			
ID	OS3Y53 HUMAN	PRELIMINARY;	PRT; 445 AA.
AC	OS3Y53		
DT	13-SEP-2005	(TREMBLrel. 31, Created)	
DT	13-SEP-2005	(TREMBLrel. 31, Last sequence update)	
DT	13-SEP-2005	(TREMBLrel. 31, Last annotation update)	
DE	START domain containing 3.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RP	NUCLEOTIDE SEQUENCE.		
RA	Kalaine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,		
RA	Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,		
RA	Phelan M., Farmer A.;		
RT	"Cloning of human full-length cDNAs in BD Creator (TM) System Donor		
RT	vector."		
RL	Submitted (May-2003) to the EMBL/GenBank/DBD databases.		
DR	EMBL; BT006964; AAP35610.1; -; mRNA.		
SQ	SEQUENCE	445 AA; 50474 MW; 62BED5C3EDA0DEF CRC64;	
Query Match		55.6%;	Score 664; DB 2; Length 445;
Best Local Similarity		56.2%;	Pred. No. 66-52;
Matches 135;	Conservative	38;	Mismatches 45; Indels 22; Gaps 5
OY	1 MNHLP----	EDMENAL-----	TGSGSSHASLRNHSINPTOLMARIESYEGREKKGISDV 51

D6		1	MSKIPRELTDLERSLPVAVASLCSSLSHSGSLSHLLPPE-----KRRLSDV	49
OY		52	RRTFCELVTFEDLLFVTLLMWIIEINVNGGIENTLEKEYMDYYSSFFDILLAVFRPKVL	111
DB		50	RRFTCFELVFETDLLFISLWIIIEINTWTGRKNLEOEIIQYNFKTSPFDIVLAFFRPSGL	109
OY		112	ILAVACRLRHMMWAIALTTAVTAFLAKITIKSLPSQCAFVYLPISTILAMIEWPL	171
DB		110	LIGVAIVQLHHMWWIAVATTVTVSSAFILVKYIIBELLSKGAFGLLPIVTSVLMALETWPL	169
OY		172	DFKVLPOEAEENRBLILVODASEAAALI-EGGSIDCGFYAPPSEAGSE-EAEEKODEK	229
DB		170	DFKVLPOEAEENRYLAAQVAVARGPLLFSGLALSEQFYSPESPFGSDNDSDEVAGKK	229
 RESULT 10				
MUN64	MOUNSE			
ID	MUN64 MOUSE	STANDARD;	PRT; 446 AA.	
AC		Q61542;		
DT		30-MAY-2000 (Rel. 39, Created)		
DT		30-MAY-2000 (Rel. 39, Last sequence update)		
DT		10-MAY-2005 (Rel. 47, Last annotation update)		
DE		MUN 64 protein (StAR-related lipid transfer protein 3) (STAR3) (START domain-containing protein 3) (ES 64 protein).		
GN		Name=Star3; Synonyms=Es64, MUN64;		
OS		Mus musculus (Mouse).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC		Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
CC		Muridea; Muridae; Murinae; Mus.		
CX		NCBI_TaxId=10090;		
NR		[1]		
RP		NUCLEOTIDE SEQUENCE.		
XP		MEDLINE=96039245; PubMed=7490069;		
RA		Tomasetto C.L., Regnier C.H., Moog-Putz C., Mattei M.-G.,		
RA		Chenard M.-P., Lidereau R., Bassot P., Rio M.-C.;		
RT		"Identification of four novel human genes amplified and overexpressed in breast carcinoma and localized to the q11-q21.3 region of chromosome 17.";		
RL		Genomics 28:367-376(1995).		
RN		[2]		
RP		NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].		
RC		TISSUE=Mammary tumor;		
RX		MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnaa.242603892;		
RA		Strauberg R.L., Feinold E.A., Grouse L.H., Derge J.G.,		
RA		Klausner B.R., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA		Aleschul S.F., Zeeberg B., Butler K.H., Schaefer C.F., Bhat N.K.,		
RA		Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,		
RA		Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA		Stepanov M., Soares M.B., Bonaldi M.F., Casavant T.P., Scheetz T.E.,		
RA		Brownstein M.J., Usdin T.B., Tothilyki S., Cantinici P., Prange C.,		
RA		Rala S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,		
RA		Boask S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA		Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulky S.W.,		
RA		Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,		
RA		Faney U., Helton E., Kettelman W., Madan A., Rodrigues S., Sanchez A.,		
RA		Whiting M., Madan A., Young A.C., Shevchenko Y., Boultard G.G.,		
RA		Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA		Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA		Butterfield Y.S.N., Kryzysinski M.I., Skalska U., Smallus D.E.,		
RA		Schmerer A., Schein J.E., Jones S.J.M., Marra M.A.;		
RT		"Generation and initial analysis of more than 15,000 full-length human		
RT		and mouse cDNA sequences."		
CC		-1- FUNCTION: Binds and transports cholesterol. Promotes		
CC		steroidogenesis in placenta and brain (By similarity).		
CC		-1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal		
CC		membrane protein (By similarity).		
CC		-1- SIMILARITY: Contains 1 START domain.		
CC		-----		
CC		This Swiss-Prot entry is copyright. It is produced through a collaboration		
CC		between the Swiss Institute of Bioinformatics and the EMBL outstation -		

CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; X62457; CAAS7834.1; -; mRNA.  
 CC EMBL; BC003313; AAH03313.1; -; mRNA.  
 CC HSSP; Q14849; 1EM2.  
 CC SMR; Q61542; 231-444.  
 CC Ensemble; ENSMUSG0000018167; Mus musculus.  
 CC MGI; MGI:1929618; Stard3.  
 CC GO; GO:0016021; C:integral to membrane; TAS.  
 CC GO; GO:0005770; C:late endosome; TAS.  
 CC InterPro; IPR000799; STAR.  
 CC InterPro; IPR002913; START\_lipid\_bd.  
 CC Pfam; PF01852; START; 1.  
 CC PRINTS; PR00978; STARPROTEIN.  
 CC SMART; SM00234; START; 1.  
 CC PROSITE; PS50848; START; 1.  
 CC Lipid transport; lipid-binding; Steroidogenesis; Transmembrane;  
 CC Transport.  
 CC FT TOPO\_DOM 1 52 Cytoplasmic (Potential).  
 CC FT TRANSMEM 53 73 Potential.  
 CC FT TOPO\_DOM 74 95 Extracellular (Potential).  
 CC FT TRANSMEM 96 116 Potential.  
 CC FT TOPO\_DOM 117 121 Cytoplasmic (Potential).  
 CC FT TRANSMEM 122 142 Potential.  
 CC FT TOPO\_DOM 143 149 Extracellular (Potential).  
 CC FT TRANSMEM 150 170 Potential.  
 CC FT TOPO\_DOM 171 446 Cytoplasmic (Potential).  
 CC FT DOMAIN 47 218 MENTAL.  
 CC FT DOMAIN 231 444 START.  
 CC SQ SEQUENCE 446 AA; 50470 MW; DBF4359604F3E1E2 CRC64;  
 Query Match 54.9%; Score 656.5; DB 1; Length 446;  
 Best Local Similarity 57.8%; Pred. No. 2.9e-51;  
 Matches 133; Conservative 33; Mismatches 47; Indels 17; Gaps 4;  
 QY 7 DMENAL-----TGSQSSHASLRNHSINPTQLMARISYGREKKISDYRRTFCVTF 61  
 Db 11 DLERSLPALASLGTSLSHSQSLSHFIPLPL-----EKRAISDVRRTFCVTF 60  
 QY 62 DLLFVTLMTIIEINLVNGIENLEKEVMQDYSSYDFILFLAVFRKVLILAVACRLR 121  
 Db 61 DLLFISLMTIIEINTNTGIRKNEQEVYHSFQSSPFIDIVLAFRRSGLLGVAVRLQ 120  
 QY 122 HMAAIALTTAVTSAFLAKYILSKLPSQGAFGVYLPIISFTLMIETWFLDPKLPQEA 181  
 Db 121 HMAVIAVTLTVSSAFILVKVILSELKSGAFGYLPLVFSVLAWLETWFLDPKLPQEA 180  
 QY 182 EENRLLIVODASERALI--PGSLSDQFVSPSEAGSE--EAEKODSEK 229  
 Db 181 EENRWYLAQAQAAVARGPLLFSGALSEGFSPSEAFASDSEDEYVAGK 230  
 RESULT 11  
 OSU2T5 RAT PRELIMINARY; PRT; 446 AA.  
 AC OSU2T5  
 DT 01-FEB-2005 (TREMBLrel. 29, Created)  
 DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)  
 DE Hypothesis 1 LOC363675.  
 GN Name=LOC363675;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Yoshlyuk S., Cantinici P., Prange C.,  
 RA Raha S.S., Loguigliano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywiński M.I., Skalka U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Heart;  
 RG NIH MGC Project;  
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC085872; AAH85872.1; -; mRNA.  
 DR SMR; Q5U2T5; 231-444.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 DR GO; GO:0015485; F:cholesterol binding; IEA.  
 DR GO; GO:0017127; F:cholesterol transporter activity; IEA.  
 DR GO; GO:0008289; F:lipid binding; IEA.  
 DR GO; GO:0006699; P:lipid transport; IEA.  
 DR GO; GO:0006694; P:steroid biosynthesis; IEA.  
 DR InterPro: IPR000799; STAR.  
 DR InterPro: IPR002913; STAR.  
 DR Pfam; PF01852; START; 1.  
 DR PRINTS; PR00978; STARPROTEIN.  
 DR SMART; SM00234; START; 1.  
 DR PROSITE; PS50848; START; 1.  
 DR Hypothetical protein.  
 SQ SEQUENCE 446 AA; 50385 MW; 19BF58B56F09722F CRC64;  
 Query Match 54.9%; Score 656.5; DB 2; Length 446;  
 Best Local Similarity 56.2%; Pred. No. 2.9e-51;  
 Matches 135; Conservative 32; Mismatches 52; Indels 21; Gaps 4;  
 QY 1 MNHLPEDMEN-----ALTSQSSHASLRNHSINPTQLMARISYGREKKISDY 51  
 Db 1 MSKLPGLADLERSLPALASLGTSLSHSQSLSHFIPLPKRYV-----VSDV 50  
 QY 52 RRTFCVFTEDLFLVTLMTIIEINLVNGIENLEKEVMQDYSSYDFILFLAVFRKVL 111  
 Db 51 RRTFCVFTEDLFLISLMTIIEINTNTGIRKNEQEVYHSFQSSPFIDIVLAFRRSG 110  
 QY 112 ILAVACRLHMAAIALTTAVTSAFLAKYILSKLPSQGAFGVYLPIISFTLMIETWFL 171  
 Db 111 ILGVAVRLQHMMAVIAVTLTVSSAFILVKVILSELKSGAFGYLPLVFSVLAWLETW 170  
 QY 172 DFKVLPQEAEEENRLLIVODASERALI--PGSLSDQFVSPSEAGSE--EAEKODSEK 229  
 Db 171 DFKVLPQEAEEENRWYLAQAQAAVARGPLLFSGALSEGFSPSEAFASDSEDEYVAGK 230  
 RESULT 12  
 OS44C3 MOUSE  
 ID OS44C3\_MOUSE PRELIMINARY; PRT; 446 AA.  
 AC OS44C3  
 DT 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DE 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
 DE clone: A630020B16 product: steroidogenic acute regulatory protein  
 DE related, full insert sequence.  
 GN Name=Stard3;



OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RT [1]  
RT NUCLEOTIDE SEQUENCE.  
RP STRAIN=C57BL/6J; TISSUE=Thymus;  
RC MEDLINE=99279233; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RX Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=11085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,  
RA Kuehl J., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L. M., Staudt F., Suzuki R., Tomita M., Wagner L., Wasth T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barin G.,  
RA Blake J., Boftelli D., Bojunga N., Carninci P., de Bonaldo M. F.,  
RA Brownstein M. J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D. A., Kamlaya M., Lee N. H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K. F.,  
RA Suzuki H., Toyooka K., Wang K. H., Weltz C., Whitaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Mikado I., Osato N., Saito R., Suzuki H., Yamana K. I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogi A., Schonbach C., Gojobori T.,  
RA Balarelli R., Hill D. P., Bull C., Hume D. A., Quackenbush J.,  
RA Schriml L. M., Kanapin A., Matsuda H., Batalov S., Beisel K. W.,  
RA Blake J. A., Bradt D., Brusic V., Chothia K., Corbani L. E., Cousins S.,  
RA Dalla E., Dragani T. A., Fletcher C. F., Forrest A., Frazer K. S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimonod S., Gustincich S., Hirokawa N., Jackson I. J., Jarvis E. D.,  
RA Kanai A., Kawai H., Kawasawa Y., Kedziński R. M., King B. L.,  
RA Konagaya A., Kurochkin I. V., Lee Y., Lenhard B., Lyons P. A.,  
RA Maglott D. R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
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RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E. S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573(2002).  
[4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
[5]

RA Carninci P., Shihata Y., Hayatsu M., Sugahara Y., Shihata K., Itoh M.,  
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.",  
RL Genome Res. 10:1617-1630(2000).  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
EX MELLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shihata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
RA Kono H., Akiyama J., Nishi K., Kitesuna T., Tashiro H., Itoh M.,  
RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa K., Irawa M., Ohara E., Wataniki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.",  
RL Genome Res. 10:1757-1771(2000).  
RN  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Thymus;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirokawa T.,  
RA Hori P., Imocani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
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RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Saeki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK041538; BAC30977.1; -; mRNA.  
DR MGI; MGI:1929618; Stard3.  
DR GO; GO:0016021; C: integral to membrane; TAS.  
DR GO; GO:0005770; C: late endosome; TAS.  
SQ SEQUENCE 446 AA; 50469 MW; D5F4359604F3E1E2 CRC64;

Query Match 54.9%; Score 656.5; DB 2; Length 446;  
Best Local Similarity 57.8%; Pred. No. 2.9e-51;  
Matches 133; Conservative 33; Mismatches 47; Indels 17; Gaps 4;

QY 7 DMENAL-----TSGQSSHASLRNTHSINPTQLMARISYEGREKKGISDVARFTCTLYTF 61  
DB 11 DLERSLPLALSLGRTSLSHSQSLSHPIPPPL-----EKRRAISDVRRFTCTCLFYTF 60  
QY 62 DLLFVYTLIMTIELLVNGGIENTLKEVWQVHYVESYDFIILANFRKRLIILAAVAORLR 121  
DB 61 DLLFISLIMTIELLVNGGIRNQLQEOEVTHVSFOSSFDIIFLAFRRISGGLLGAVALRLQ 120  
QY 122 HMMVIALTTVNTASAFILAKVTLISKLFSGAGCYVLPIISFIILAVETMFLDFKVLPOEAE 181  
DB 121 HMMVIAVTVLVSSAFILYKVLISLSELSGAGCYLLPIVSFVLALLETMFLDFKVLPOEAE 180  
QY 182 ENBRLLIYQDASERAAAL-PCGLSDQGFYSPSESEAGSE-BAEKKDSEK 229  
DB 181 EBRWLLAQAQAAVARGPFLIFSGALSSCGCY9PPESFAGSDNESDEVTGKK 230

RESULT 13  
MUN64 BRARE  
AC 09DRES4; OS6FH03; STANDARD; PRT; 448 AA.  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 01-FEB-2005 (Rel. 46, Last sequence update)  
DE MUN64-like protein (START domain-containing protein 3).  
GN Name=stard3; Synonyms=mun64;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;

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OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=AB;
RG NIH - Zebrafish Gene Collection (ZGC) project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE OF 210-448.
RA PubMed:1106158; DOI=10.1016/S0303-7207(00)00316-6;
RA Bauer M.P., Bridgman J.T., Langanau D.M., Johnson A.L., Goetz F.W.;
RT "Characterization of steroidogenic acute regulatory (Star) protein
RT structure and expression in vertebrates."
RL Mol. Cell. Endocrinol. 168:119-125(2000).
CC -1- FUNCTION: Binds and transports cholesterol. Promotes
CC steroidogenesis (by similarity).
CC -1- SIMILARITY: Contains 1 STAR domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BC056766; AAH56766.1; -; mRNA.
DR EMBL; AF258786; AAG28603.1; -; mRNA.
DR HSSP; O14849; 1EM2.
DR SMR; Q9DE54; 232-443.
DR Ensembl; ENSDARG0000017809; Danio rerio.
DR ZFIN; ZDB-GENE-001120-2; starc3.
DR InterPro; IPR000799; STAR.
DR InterPro; IPR002913; STAR_lipid_bd.
DR Pfam; PF01852; START; 1.
DR PRINTS; PR00978; STARPROTEIN.
DR SMART; SM00234; START; 1.
DR PROSITE; PS00848; START; 1.
DR Lipid transport; lipid-binding; Steroidogenesis; Transport.
FT DOMAIN 232 445 YSPESLAGSE -> PGRPVPRPVR (in Ref. 2).
FT CONFLICT 210 220
SQ SEQUENCE 448 AA; 50751 MW; 716A18C127B59C5D CRC64;

Query Match 52.9%; Score 632; DB 1; Length 448;
Best Local Similarity 70.9%; Pred. No. 5,1e-49;
Matches 127; Conservative 18; Mismatches 32; Indels 2; Gaps 2;

QY 44 EKKGISVRRTEFLFTYFDLLFTLMTIELNNGGENTLEKEVMQDYSSYFDLFTL 103
DB 43 ERKAFSDVRRTFCLFTYFDLLFTLMTIELNISKSISWNSLENEVHYNFKSSFFDLFTL 102
QY 104 AVRFPKVLLIAYVAVCRLRHMAIALTTAVTSAPFLAKVILSKLFSQAGFVLPILISFIL 163
DB 103 AVRFPLCLQGYAARLRHMAIALTTLVTTAPLIAVILSDLFSGVAFVLPITSFV 162
QY 164 AWIETWFLDFKVLPOEAKEEN-RLLIYQDASERAAI-PCGLSDGQFYSPSEAGSEE 220
DB 163 AWIETWFLDFKVLTOEADEDERVYLAANACAPAPLICPRPVSQGYSPSEIAGSED 221

RESULT 14
QAS943.TETNG PRELIMINARY; PRT; 444 AA.
ID QAS943.TETNG
AC QAS943;
DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
DE Chromosome 3 SCAF14700, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GTENG0022066001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percormorpha; Tetradontiformes;
OC Tetradontidae; Tetradontidae; Tetradon.

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OX NCBI_TaxID=99863;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Niclaud S., Jaife D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthonard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skali Z., Catolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brotier P., Coutanceau J.P., Guzy J.,
RA Paria G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volt I., Guigo R., Zody M.C., Nesitov U.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schacher V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Croallie H.;
RT "genome duplication in the teleost fish Tetradon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01014700; CAG02839.1; -; Genomic DNA.
FT NON_TER 1 1
FT NON_TER 444 444
SQ SEQUENCE 444 AA; 50312 MW; 0A2E1D687EDB2C41 CRC64;

Query Match 49.1%; Score 586.5; DB 2; Length 444;
Best Local Similarity 55.2%; Pred. No. 7.2e-45;
Matches 122; Conservative 30; Mismatches 42; Indels 27; Gaps 5;

QY 12 LTGSGSHASLRNHS-----INTQLMARIESVEGKEKGISVRRTEFLFTYFDLFT 67
DB 5 ISMNSHSTSLSLPSPYFVPPA-----ARKTISVRRTEFLFTYFDLFTS 52
QY 68 LMTIELNNGGIENTLEKEVMQDYSSYFDLFLAVRFKVLIIAYVAVCRLRHMAIAL 127
DB 53 LMTIELNNSLSKESLNHEVHYDYRSSFFDLFLAVRFPLCLQGYAARLRHMAIAL 112
QY 128 LTTAVTSAPFLAKVILS-----KLFSQAGFVLPILISFILAWIETWFLDFKVL 178
DB 113 VTTLVTCVFLVXLTILSNNAAGSDNLISQNAFGVLPITSFVAVLWETWFLDFKVL 172
QY 179 EAEENRLIYQDAS-ERAAI-PCGLSDGQFYSPSEAG 217
DB 173 EADDERAYLAANVASCERSPMIYPRVSDQFYSPSEIAG 213

RESULT 15
QSRB70.PONPY PRELIMINARY; PRT; 501 AA.
ID QSRB70.PONPY
AC QSRB70;
DT 01-FEB-2005 (TEMBLrel. 29, Created)
DT 01-FEB-2005 (TEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469E1839.
DE Name=DKFZp469E1839;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Ottemaeijder B., Obermaier B., Deuschenebauer S., Schaidp A.,
RA Neues H.W., Weil B., Amid C., Oesinger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR858784; CAH90990.1; -; mRNA.

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